

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2005, 06:04:49 ; Search time 52 Seconds
(without alignments)
458.880 Million cell updates/sec

Title: US-10-080-522-1
Perfect score: 1308
Sequence: 1 MQTCPLAPGHVSQALGTLT.....PLGALELLSPOQLFPYADP 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103.5	7.9	550	2 S64725	probable lipoprote
2	94.5	7.2	393	2 T07167	probable isocitrat
3	90.5	6.9	271	2 T36895	probable membrane
4	90	6.9	1088	2 H96747	unknown protein T1
5	89	6.8	798	2 A12053	competence protein
6	86.5	6.6	929	2 A44048	genome polypotein
7	86	6.6	493	1 S51574	mocr protein - Rhi
8	85.5	6.5	420	2 A82699	conserved hypotet
9	85.5	6.5	468	1 B46114	glycoprotein gp13
10	85.5	6.5	2303	1 GNNVTP	genome polypotein
11	85.5	6.5	2303	2 S13554	genome polypotein
12	84.5	6.5	289	2 A83608	polyamine transpor
13	83.5	6.4	468	1 VGBEEH	glycoprotein gp13
14	83	6.3	550	1 VGBE18	glycoprotein E - h
15	83	6.3	4436	2 E11086	hypothetical prote
16	82.5	6.3	233	2 T15620	hypothetical prote
17	82.5	6.3	288	2 A55737	PD-1 protein - hum
18	82.5	6.3	636	2 T47236	hypothetical prote
19	82	6.3	398	2 T46475	hypothetical prote
20	81	6.2	450	1 FOLJFP	gag polypotein -
21	81	6.2	450	1 S23819	gag protein - feli
22	80.5	6.2	312	2 C87562	conserved hypotet
23	80.5	6.2	541	2 T48811	hypothetical prote
24	80.5	6.2	1240	2 T03097	CDO protein - huma
25	80.5	6.2	2301	1 GNNVTM	genome polypotein
26	80.5	6.2	2303	1 GNNVTM	genome polypotein
27	80	6.1	290	2 T09260	aquaporin-like tra
28	79	6.0	407	2 B70962	hypothetical prote
29	79	6.0	950	2 T51134	ionotropic glutama

30 78 6.0 204 2 T51012 hypothetical prote
31 77.5 5.9 390 1 Q0BE77 glycoprotein I pre
32 77.5 5.9 834 2 S66498 M-sena F protein p
33 77 5.9 99 2 C46518 Ig L1 chain V regi
34 77 5.9 124 2 S08640 hypothetical prote
35 77 5.9 287 2 S60455 transmembrane prot
36 77 5.9 289 2 S33617 trg-31 protein - g
37 77 5.9 303 2 A40807 membrane glycoprot
38 77 5.9 364 2 H75466 lipopolysaccharide
39 77 5.9 442 1 XUBRVS 3-phosphoshikimate
40 77 5.9 910 2 D75524 alpha-dextran endo
41 77 5.9 3097 2 T00021 DN-cadherin - frui
42 77 5.9 26926 1 I38344 titin, cardiac mus
43 76.5 5.8 351 2 S39603 class I histocompa
44 76.5 5.8 666 2 H83943 transketolase tkt
45 76.5 5.8 835 2 S40140 ribonucleoside-dip

ALIGNMENTS

RESULT 1
S64725
probable lipoprotein uxpa precursor - Pseudomonas putida
C;Species: Pseudomonas putida
C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 09-Jul-2004
C;Accession: S64725; S47503
R;de Groot, A.; Kriliger, J. J.; Filloux, A.; Tommassen, J.
Mol. Gen. Genet. 250, 491-504, 1996
A;Title: Characterization of type II protein secretion (xcp) genes in the plant growth-
A;Reference number: S64724; MUID:96186881; PMID:8602167
A;Accession: S64725
A;Molecule type: DNA
A;Residues: 1-550 <DEG>
A;Cross-references: UNIPROT:Q52289; EMBL:X81085; NID:g3293032; PIDN:CAA56977.1; PID:g53
C;Genetics:
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-550/Product: probable lipoprotein uxpa #status predicted <NAT>

Query Match 7.9%; Score 103.5; DB 2; Length 550;
Best Local Similarity 23.2%; Pred. No. 0.17;
Matches 72; Conservative 42; Mismatches 118; Indels 79; Gaps 16;
QY 2 QTCPLAPGHVSQA-LGTLFLAA-----SLSAQN-EGWDSPTCTGVSVVS 46
Db 90 QLAPLLDAGRADEANLGGYAVLGALEQLRGEAGAGNSLTLENGQWNG----SGLAYLT 145
QY 47 WGVNTVMSNCINAFSHVNIKRA--HGQESAIFNEVAPGYFSR-----DGWQ 92
Db 146 QGESGVQSGQLLGSEARVSSDERVLPQSAALYRQASATTLGAGLADEORQALGLEPLQ 205
QY 93 LQVQGVGAQLVTKG-----ARDSHAGLYMWH---LVGHORNNRQVTLVSGASPOSAP-- 142
Db 206 LFERGG-ARIAVGVTDTPYAQDKASLKYQALLFPVFOQAREADLVVALADVGTGPG 264
QY 143 -----DTGFWPVPVAVTAVFILLVALVMPAW-----YRCRC-----SQQ 176
Db 265 WLAERLPAIDLLLCARGQDLWPTPVQATQASGRVP-VLFAGCRGSGAFRLRCQQVAGQW 323
QY 177 REKKFF-----LLEPMQVAALRAGAQQGLSPASAEIWTDPDSEPTPR-PLALVFKPSPL 230
Db 324 QFEGREFFTFEQTLSPPAQVRAGQLOAQNLQQRAGHAWL--DOPLARAPQALWRRDRTRG 381
QY 231 GALELLSPOQL 241
Db 382 GSWDRLLHQA 392

RESULT 2
T07167
Probable isocitrate dehydrogenase (NAD) (EC 1.1.1.41) chain 1 - tomato
C;Species: Lycopersicon esculentum (tomato)

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C/Accession: T07167
R/Tahiri-Alaoui, A.; Avrova, A.; Antoniw, J.F.
submitted to the EMBL Data Library, January 1998
A/Description: A putative mitochondrial isocitrate dehydrogenase from tomato roots up-regulated in response to wounding

C/Reference number: 215974
A/Accession: T07167
A/Status: translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-393 <ANT>
A/Cross-references: UNIPROT:O82004; EMBL:Y16126; PIDN:CAA76076.1
A/Experimental source: cultivar Early Mech; root
C/Superfamily: 3-isopropylmalate dehydrogenase
C/Keywords: oxidoreductase

Query Match 7.2%; Score 94.5; DB 2; Length 393;
Best Local Similarity 23.8%; Pred. No. 0.76;
Matches 51; Conservative 30; Mismatches 68; Indels 65; Gaps 9;

QY 63 HVNIKILRAHGOESAIFFNEVAPG---YFSRDGWLQVGGVQAOLVIKGR--DSHAGL-Y 115
DB 94 HGDMEKVASGDVDCISN---PGRKNVWFKEGKWTVPVGGVSSLNVLQRLKELDLIASLVH 150
QY 116 MHWLVGHQRNNRQVTL-----EVSQAEPQSA-----DT 144
DB 151 CFNLKGLPTRHENVDIVIRENTEGEYSGLHEVVPGWESLKVMTKFCSERIAKVAFYE 210
QY 145 GFWPVPVAVTAVF---ILLVALVMAFYRCRCQORREKFFLLEPQMKVAALRAGAQOG 201
DB 211 AYLNNRKVTAVAHKANIMENLLMVYFESC-----RRDKQITLG----- 250
QY 202 LRSASAEMLTPDSEPTPRPLALVPKPSPLGALEL 235
DB 251 -SSTMRELWTTVACNLYSQSLNMLMWSPLISTEI 283

RESULT 3
T36885
probable membrane protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T36885
R/Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A/Reference number: Z21617
A/Accession: T36885
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-271 <MUR>
A/Cross-references: UNIPROT:Q95218; EMBL:AL109848; PIDN:CAB52846.1; GSFDB:GN00070; SCOE
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOEDB:SGI51.22c
C/Superfamily: hemolysin homolog yqxC

Query Match 6.9%; Score 90.5; DB 2; Length 271;
Best Local Similarity 25.1%; Pred. No. 1.1;
Matches 51; Conservative 21; Mismatches 60; Indels 71; Gaps 8;

QY 83 PGVFSRDGWLQVGGVQAQ---LVITKGR-----DSH 111
DB 63 PDVVSRGHKL--AGALAAFPVHGLVVEGRALDAGASTCGFTDVLRLRAGAAHVAVDVG 120
QY 112 AGLYMWHL-----VGHQRNNRQVTLVSGABEQSAPDTGFWPVPVAVTAVTIFILVALV 164
DB 121 YGQLANSLRQDERVTVDKRTNVRELTPDAIDG-----PVDLVVGDLSFIPLALV 170
QY 165 MFAFYRCRCQORREKFFLLEPQMKV-----AALRAGAQOGLSPASAEELWT 211
DB 171 LPALVRC---TRGADLVMMVKQFVGVGKERLGGVVRSAQLRAEAVRGVAKRWELGL 227
QY 212 PDSEPTPRPLALVPKPSPLGALEL 234

A:Gene: comE

Query Match 6.8%; Score 89; DB 2; Length 798;
Best Local Similarity 21.6%; Pred. No. 5.4;
Matches 44; Conservative 33; Mismatches 73; Indels 54; Gaps 9;
Qy 40 EGVSVSVNGENTVMSNCISNAFHV-----NIKLRAGHGSIAIFNEVAPCFYFRDGMW 92
Db QGVNQIDWAIATDFORNNNDAMLEVLQRLAKNFYAYATNKENSADQAIPOI----- 658
Qy 93 LQVGGVQAOLVKGARDSHAGLYMHLVGHQNNR-----QVTLVSVGAEPQSAP---DT 144
Db LQKQKGIYVOLLVPGV-QTINLSTVAQLINEOPMQLQMGOSWLLVGVDPKEVERIMKA 717
Qy 145 GFWPVPVAVTAVFILLVALVFAVRCRCRQORREKFFLEPQMKVA---ALRAGAQQ 201
Db GGMFSPQVL-----W-----CNAESLKDLYMMLKPVQVIASSGSLESTVLS 759
Qy 202 LSRASAEI-----WTPDSE 215
Db LSKTSTKVFVTAQDGAIQMPNGE 783

RESULT 6

A44048
genome polyprotein - Vilyuisk virus (strain V-1) (fragment)
C:Species: Vilyuisk virus
C:Date: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 07-Feb-1997
R:Pritchard, A.E.; Strom, T.; Lipton, H.L.
Virology 191, 469-472, 1992
A:Title: Nucleotide sequence identifies Vilyuisk virus as a divergent Theiler's virus.
A:Reference number: A44048; MUID:93033144; PMID:1413519
A:Accession: A44048
A:Molecule type: genomic RNA
A:Residues: 1-329 <PRI>
A:Cross-references: GB:M94868
C:Superfamily: foot-and-mouth disease virus genome polyprotein
C:Keywords: polyprotein

Query Match 6.6%; Score 86.5; DB 2; Length 929;

Best Local Similarity 27.0%; Pred. No. 11;
Matches 27; Conservative 16; Mismatches 34; Indels 23; Gaps 5;
Qy 61 FSHVNIKL-RAHGOESAIFFN-EVAPGYFSRDGWLQVGGVQAOLVKGARDSHAGLYM 117
Db FSHRVLPALAGEHGVGFATLRHHYLAKEGHRVQVQCNASQF-----HAGSLIV 275
Qy 118 HL-----VGHQNNRQVTLVSVGAEPQSAPDTGF 146
Db FLAPEFYTGTVATSGQEPNKFVFLMDTTWQEPQAAP-TGF 314

RESULT 7

S51574
mocr protein - Rhizobium meliloti
C:Species: Rhizobium meliloti
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R:Rosbach, S.; Kulp, D.A.; Rossbach, U.; de Bruijn, F.J.
Mol. Gen. Genet. 245, 11-24, 1994
A:Title: Molecular and genetic characterization of the rhizopine catabolism (mocrABRC) gene
A:Reference number: S51569; MUID:95147842; PMID:7845353
A:Accession: S51574
A>Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-493 <ROS>
A:Cross-references: UNIPROT:P49309; EMBL:X78503; NID:G468758; PID:G468764
C:Genetics:
A:Gene: mocr
C:Superfamily: hypothetical protein b1439

Query Match 6.6%; Score 86; DB 1; Length 493;

Best Local Similarity 26.0%; Pred. No. 5.8;
Matches 53; Conservative 20; Mismatches 65; Indels 66; Gaps 11;

Qy 60 AFSHVNIKLRAHGOESAIFFNEVA--PGY-----PSRDGWLQVGGVQAOLVKGARDSHA 112
Db SLSSRGMRMAAQPRDRTIPDRIAEHPGYPEIKAFPFSTW-----ARLKRHARYSHE 147
Qy 113 GLYMHVILV-GHQNNRQVTLVSVGAEPQSAPDTGFWPVPAVVTAVFILLVALVMPA---- 167
Db DLYGVHVTGHPR-----LKAATAEYLRA-SRCVECAPEQVIVNGTQAALDILARMLV 200
Qy 168 -----MYRCRCRQORREKFFLEPQMKVAALRAGAQQGLSRASAEI-----WTP 212
Db DEGDICW-----MEEPGY-----IGAQNLSLSAGAKLPLPVERDGNLS 239
Qy 213 DSEPTPRPLALVFKPS---PLGAL 233
Db EDETRPSRPIIFVTPSCQWFLGCL 263

RESULT 8

A82699
conserved hypothetical protein XF1304 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82699
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82615; MUID:20385717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82699
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <SIM>
A:Cross-references: UNIPROT:Q9PDS5; GB:A8003963; GB:A8003949; NID:G9106285; PIDN:AAF84;
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carrer, as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Froil J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Lai Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawas M.; Tshako, M.H.; Vallada, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, M.; Verjovski-Almeida, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A:Contents: annotation
A:Reference number: A59328
C:Genetics:
A:Gene: XF1304

Query Match 6.5%; Score 85.5; DB 2; Length 420;

Best Local Similarity 21.1%; Pred. No. 5.4;
Matches 59; Conservative 36; Mismatches 110; Indels 75; Gaps 11;
Qy 10 GHVSQAL-GTLLFLAASLSAQNGWDSPICTEGVSVSVSGENTVMSNCISNAFHVNIKL 68
Db GTTAQRLEASLVALSQQLGUDCEPWSNP--TGLISFSDPAKAIGSSDITRVI----- 83
Qy 69 RAHGOESAIFFNEVAPGYFSRDGWLQVGGVQAOLVKGARDSHAGLYMHLVGHQNNRQ 128
Db -----RLAPG--ENDLYKLSVADNVAQVAGSRMSISQHTALRLDRELDPRS 130
Qy 129 VTLVSVGAEPQSAPDTGFWPV--AVVTAVFI-LLVALVMPFVRCRCRQORREKFFLL 185
Db -----TQYDTHRAATR 180
Qy 186 EPQMKVVALRAG-----AQQGLSRASAEIWPDS 214
Db EASEALAAALGFVATLVATLIGPINLNTVIAISVVVLLPGMSLTNAVNELSSQHWVSGT 240


```

QY      2  QTCPLAFPHGVHQSALGTLTLFLAASLSAQNECHDSP-----ICTEGVYVSVHGENTVMS 54
DB      34  QSTP-ATPHTPNLTAAHGAQSDNTNANGTESTHSHETTTCTKSLISVPYKSVDMN 92
QY      55  CNISNAFSHVNIKLRAHGOESAIFNEVAPG----YF-----SRDG 90
DB      93  CTTSVGVNYSYRLEIYLNORTPFGCTPGDEENYINHNATKDQTLTLLFSTAERKKSRRG 152
QY      91  WQLOV-----OGGVA-OLVVIKGARDSHAGLYMMHLV---GHORNNRV 129
DB      153  GOLGVLPIDBLPKRQFNLPHTHEGGFKFPLTIKSDVWRTAGIYVMSLYAKNGTLVNSTSV 212
QY      130  TLEVSQA 136
DB      213  TVSTYNA 219

RESULT 14
VGBE18
glycoprotein E - human herpesvirus 1
N:Alternate names: US8
C:Species: human herpesvirus 1
C:Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C:Accession: A03733; A45696
R:McGoch, D.J.; Dolan, A.; Donald, S.; Rixon, F.J.
J. Mol. Biol. 181, 1-13, 1985
A:Title: Sequence determination and genetic content of the short unique region :
A:Reference number: A06656; MUID:85160822; PMID:2984429
A:Accession: A03733
A:Molecule type: DNA
A:Residues: 1-550 <MCG>
A:Cross-references: UNIPROT:P04488; GB:X02138; NID:G59865; PIDN:CAA26062.1; PID
A:Experimental source: strain 17
R:Georgopoulou, U.; Michaelidou, A.; Roizman, B.; Mavromara-Nazos, P.
J. Virol. 67, 3961-3968, 1993
A:Title: Identification of a new transcriptional unit that yields a gene product
A:Reference number: A45696; MUID:93287213; PMID:8389914
A:Accession: A45696
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 438-550 <GEO>
A:Cross-references: GB:S62895; NID:g386127; PIDN:AAB27080.1; PID:g386128
A:Experimental source: R35
A:Note: sequence extracted from NCBI backbone (NCBIN:133646, NCBIP:133647)
C:Superfamily: herpesvirus glycoprotein E
C:Keywords: glycoprotein
C:Keywords: Glycoprotein
P:124,243,501/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.3%; Score 83; DB 1; Length 550;
Best Local Similarity 25.4%; Pred. No.12;
Matches 53; Conservative 16; Mismatches 62; Indels 78; Gaps 11;

QY      80  EVAPGVFSRDMQLOVQGGVAOLVIKGARDSHAGLYMW-----HLVGH-----QR 124
DB      330  EFPVG-----LAWQASVNLFRDASPOHSGLYLCVVYVNDHIFANGHITISTAAQY 381
QY      125  NNRQV-----TLEVSAEPOSADPTGFWPVPVAVTAVFILLVALVMEFWYR 170
DB      382  RNAVVEQPLQRFQADLAETPETHVGPAPHPPTHGALRLGAVNGAA-LLLSALGLSVWAC 440
QY      171  CRCSDORREKKFFLELPQMVKVAALRAGAQQGLSR-----ASAEL---WTPDSE----- 215
DB      441  MTCWRR-----AWRAKVSRAQKGPYIRVADSELYADWSSDSEGERDQ 485
QY      216  -----PTPRPLALVPKPSPLGA-LELLSP 238
DB      486  VPLWAPPERP----DSPSTNGSGFEILSP 510

RESULT 15
E71086
hypothetical protein PH0954 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii

```

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C;Accession: E71086
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:98344137; PMID:9679194
 A;Accession: E71086
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-4436 <KAW>
 A;Cross-references: UNIPROT:O58559; GB:AP000004; NID:G3236131; PIDN:BAA30051.1; PID:d103
 A;Experimental source: strain OT3
 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C;Genetics:
 A;Gene: PH0954

Query Match 6.3%; Score 83; DB 2; Length 4436;
 Best Local Similarity 23.0%; Pred. No. 1.4e+02;
 Matches 37; Conservative 24; Mismatches 58; Indels 42; Gaps 8;
 Qy 34 DSPICTEGVSVS-----WGENTVMSCNISNAFSHVNIKLR-----HGQE 74
 Db 300 DDPDLSNNLAEGVWPGDYWENASINNLIPEFASINFKVTTTSKIPSAKVLLRNGVE 359
 Qy 75 SAI-----FNEVAPGYFSRDGMQLQVQGG--VAQLVIKGARDSHA-----GLYMMHLV 120
 Db 360 EKIEYLSFYNGIAEGEIS--W--LVQGGNYTLALLVEGKGIDINSNNIYLLGNYNPLP 414
 Qy 121 GQRNROVTL-----EVSQAEFQSPADTGFVFPVAVTAVF 157
 Db 415 NFEVGNYSIDLPTCVDSTGEVRVNVVTSTANWSIPVRLTLVY 455

Search completed: October 17, 2005, 07:13:18
 Job time : 55 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2005, 06:04:49 ; Search time 121 Seconds
(without alignments)
1049.551 Million cell updates/sec

Title: US-10-080-522-1

Perfect score: 1308

Sequence: 1 MQTCPLAPGHVSQALGTL.....PLGALELLSQPLFPYAADP 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1308	100.0	248	1 SCTM_HUMAN
2	382	29.2	192	2 Q211W8
3	376.5	28.8	201	2 Q6P781
4	358	27.4	201	2 Q6AYS0
5	327.5	25.0	211	2 Q8VDU7
6	326	24.9	212	1 SCTM_MOUSE
7	325	24.8	212	2 Q9D966
8	324	24.8	212	2 Q8CE38
9	103.5	7.9	550	2 Q52289
10	102.5	7.8	506	1 SHS1_BOVIN
11	101	7.7	334	2 Q8XZ59
12	98.5	7.5	304	2 Q8BPN5
13	98	7.5	542	2 Q8NHS5
14	97	7.4	894	2 Q5V5F7
15	96.5	7.4	550	2 Q8BP09
16	96	7.3	442	2 Q9H8B3
17	96	7.3	917	2 Q6NNX3
18	96	7.3	969	2 Q86K66
19	95	7.3	1140	2 Q80T91
20	94.5	7.2	393	2 Q82004
21	94.5	7.2	690	2 Q62AS3
22	94.5	7.2	690	2 Q63JU4
23	91.5	7.0	864	2 Q6P779
24	91.5	7.0	1260	2 Q7NR05
25	91	7.0	6620	2 Q96AA2
26	90.5	6.9	271	2 Q9S218
27	90	6.9	1088	2 Q9C9D7
28	89	6.8	798	2 Q9YVU4
29	88.5	6.8	352	2 Q63NV8
30	88	6.7	327	2 Q8RYG9
31	87.5	6.7	298	2 Q804R4

32	87.5	6.7	372	2	Q90Y50	Q90Y50 brachydanio
33	87.5	6.7	645	2	Q8MJZ5	Q8MJZ5 pan troglod
34	87.5	6.7	947	2	Q8BKK7	Q8BKK7 mus musculus
35	87	6.7	259	2	Q82SL8	Q82SL8 nitrosomona
36	86.5	6.6	395	2	Q88LS8	Q88LS8 pseudomonas
37	86.5	6.6	420	2	Q87DX4	Q87DX4 xylella fas
38	86.5	6.6	930	2	Q02472	Q02472 theiller's e
39	86	6.6	493	1	MOCR_RHIME	P49309 rhizobium m
40	86	6.6	508	2	Q80ZD5	Q80ZD5 rattus norv
41	85.5	6.5	407	2	Q9D2J4	Q9D2J4 mus musculus
42	85.5	6.5	418	2	Q8MI84	Q8MI84 pongo pygma
43	85.5	6.5	420	2	Q9PDS5	Q9PDS5 xylella fas
44	85.5	6.5	430	2	Q8MI85	Q8MI85 pongo pygma
45	85.5	6.5	922	2	Q88495	Q88495 theiller's e

ALIGNMENTS

RESULT 1

ID	SCTM_HUMAN	STANDARD;	PRT;	248 AA.
AC	Q8WV6; Q00466;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Secreted and transmembrane protein 1 precursor (Protein K12).			
GN	Name=SECTM1;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]	SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.			
RP	MEDLINE=98149980; PubMed=9480746; DOI=10.1006/geno.1997.5151;			
RA	Slentz-Kesler K.A., Hale L.P., Kaufman R.E.;			
RT	"Identification and characterization of K12 (SECTM1), a novel human			
RT	gene that encodes a Golgi-associated protein with transmembrane and			
RT	secreted isoforms."			
RL	Genomics 47:327-340(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[3]			
RP	INTERACTION WITH CD7.			
RX	MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431;			
RA	Lyman S.D., Escobar S., Rousseau A.-M., Armstrong A., Fanslow W.C.;			
RT	"Identification of CD7 as a cognate of the human K12 (SECTM1)			
RT	protein."			
RL	J. Biol. Chem. 275:3431-3437(2000).			
CC	-1- SUBUNIT: Interacts with CD7.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein (Probable). Also			

CC found as secreted.
 CC TISSUE SPECIFICITY: Detected at the highest levels in peripheral
 CC blood leukocytes and breast cancer cell lines. Found in leukocytes
 CC of the myeloid lineage, with the strongest expression observed in
 CC granulocytes and no detectable expression in lymphocytes.

CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL; U77643; AAC52044.1; -.
 CC EMBL; BC017716; AAH17716.1; -.
 CC Genbank; HGNC:10707; SECTM1.
 CC H-InvDB; HIX0014254; -.
 CC MIM; 602602; -.
 CC InterPro; IPR007110; Ig-like.
 CC Signal; Transmembrane.

FT SIGNAL 1 28 Potential.
 FT CHAIN 29 248 Secreted and transmembrane protein 1.
 FT DOMAIN 29 145 Extracellular (Potential).
 FT TRANSMEM 146 166 Potential.
 FT DOMAIN 167 248 Cytoplasmic (Potential).
 FT DISULFID 38 55 Potential.
 FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 191 191 V -> F (in Ref. 2).
 SQ SEQUENCE 248 AA; 27039 MW; 21E3066B67920487 CRC64;

Query Match 100.0%; Score 1308; DB 1; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.4e-107;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MOTCLAPPGHVSQALGTLFLAASLSAQNCGWDSPTCTEGVSVSGWNTVMSCNISNA 60
 Db 1 MOTCLAPPGHVSQALGTLFLAASLSAQNCGWDSPTCTEGVSVSGWNTVMSCNISNA 60
 Qy 61 FSHVNIKLRAHQESAI FNEVAPGFYFSDRGWQLOVGGVAQLVTKGARDSHAGLYMHLV 120
 Db 61 FSHVNIKLRAHQESAI FNEVAPGFYFSDRGWQLOVGGVAQLVTKGARDSHAGLYMHLV 120
 Qy 121 GHQNNRQVTLVSGAEPOSADPTGFVPVAVTAVFILLVALVNFAYRCRCQORREK 180
 Db 121 GHQNNRQVTLVSGAEPOSADPTGFVPVAVTAVFILLVALVNFAYRCRCQORREK 180
 Qy 181 KFFLLEPMKVAAALRAGAOQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALLSPQ 240
 Db 181 KFFLLEPMKVAAALRAGAOQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALLSPQ 240
 Qy 241 LFPYAADP 248
 Db 241 LFPYAADP 248

RESULT 2

Q921W8 Q921W8 PRELIMINARY; PRT; 192 AA.
 ID Q921W8
 AC Q921W8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CDNA sequence BC010462.
 GN Name=BC010462;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010462; AAH10462.1; -.
 DR MGD; MGI:2384805; BC010462.
 DR SMART; SM00409; IG; 1.
 SQ SEQUENCE 192 AA; 21438 MW; 13D8989D3F07AE1F CRC64;

Query Match 29.2%; Score 382; DB 2; Length 192;
 Best Local Similarity 43.6%; Pred. No. 9.3e-26;
 Matches 85; Conservative 31; Mismatches 55; Indels 24; Gaps 6;

Qy 1 MOTCLAPPGHVSQALGTLFLAASLSAQNCGWDSPTCTEGVSVSGWNTVMSCNISNA 60
 Db 1 MMTCP-SVPAIPTLWLFSLILLVLSNAQNKSHDNFICTEGILSVPRGNPAVMTCSINT 59
 Qy 61 FSHVNIKLRAHQESAI FNEVAPGFYFSDRGWQLOVGGVAQLVTKGARDSHAGLYMHLV 120
 Db 60 FTDVTQLSANGKDKTIFDKKPGQNFSGRWELQVGGQALVTKQDDHTGIYWLQHL 119
 Qy 121 GHQNNRQVTLVSGAEPOS--APTGFV-----PVP-----AVVTAVFILL 160
 Db 120 GRQRCYKNTLNT--LEPSNEDKVPDTTLTSPFDHAKSPIEGKPGTLVGVTIVFILG 177
 Qy 161 VA-LVMFAWYRCRCS 174
 Db 178 VAGFITFIYRHRSS 192

RESULT 3

Q6P781 Q6P781 PRELIMINARY; PRT; 218 AA.
 ID Q6P781
 AC Q6P781
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein MGC72571.
 GN Name=MGC72571;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Schein J.E.,
RA	Jones S.J., Marra M.A.,
RT	"generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]
RC	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RL	Director MGC Project;
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR	ENBL; BC078937; AH78937.1; -
DR	Interpro; IPR007110; Ig-like.
KW	Hypothetical protein.
DQ	SEQUENCE 201 AA; 22762 MW; 790B959BA483B98 CRC64;
SQ	
Query Match 27.4%; Score 358; DB 2; Length 201;	
Best Local Similarity 41.8%; Pred. No. 1.3e+23;	
Matches 79; Conservative 25; Mismatches 61; Indels 24; Gaps 4;	
QY	16 LGTLFLPLASLSAQNGWDSPICTEGVSVSGWENTVMSCNINAFSHVNIKURAHGOES 75 ::: :: :: :: :: :: :: :: :: :: :: :: :::
Db	15 LFSILVLVVSLNAQNKSQWRPCTENIVSYVGRPAVMSCNISNTFTDVTIQLTAHGKDR 74 ::: :: :: :: :: :: :: :: :: :: :: :: :::
QY	76 AIFNEVAPGVESRDGQLOVGGAQAOLVTKGARDSHAGLYMHHLVGHQRNNROVTVLEVS 135 :: :: :: :: :: :: :: :: :: :: :: :: :::
Db	75 TIPKKPKQGNSWSGWELHVGQAOLVKDAODHRGIYLMWLQHGRQRYRITLVNS- 133 ::: :: :: :: :: :: :: :: :: :: :: :: :::
QY	136 AEPPQ-----SAPD----TGFWPVPVAVTAVFILLVA-----LVMFAWYRCRC 173 :: :: :: :: :: :: :: :: :: :: :: :: :::
Db	134 -EPSNEDKVTDTRLFTSLPDQVKSSLEAKPGTGMGVIIIAVLALGPVGLALICYRHCRS 192 :: :: :: :: :: :: :: :: :: :: :: :: :::
QY	174 SQORREKF 182 ::: :: :: :: :: :: :: :: :: :: :: :: :::
Db	193 QKPWWYRF 201 ::: :: :: :: :: :: :: :: :: :: :: :: :::
RESULT 5	
Q8VDU7	PRELIMINARY; PRT; 211 AA.
ID	Q8VDU7
AC	Q8VDU7; 20, Created)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
GN	Sectm1 protein.
OS	Name=Sectml; (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
ON	[1]
RP	SEQUENCE FROM N.A.
RP	STRAN=CZECH II; TISSUE=Mammary tumor;
RX	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieff F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udwin T.B., Toshlyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Schein J.E.,
RA	Jones S.J., Marra M.A.,
RA	"generation and initial analysis of more than 15,000 full-length human
RA	and mouse cDNA sequences.";
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA	[2]
RC	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RL	Director MGC Project;
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR	ENBL; BC078937; AH78937.1; -
DR	Interpro; IPR007110; Ig-like.
KW	Hypothetical protein.
DQ	SEQUENCE 201 AA; 22762 MW; 790B959BA483B98 CRC64;
SQ	

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II.; TISSUE=Mammary tumor;
 RA Strauberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020159; AAH20159.1; -;
 DR MGD; MGI:1929083; Sectm1.
 DR SMART; SM00409; IG; 1;
 SQ SEQUENCE 211 AA; 23433 MW; 9B6FB436592BB2B8 CRC64;

 Query Match 25.0%; Score 327.5; DB 2; Length 211;
 Best Local Similarity 40.0%; Pred. No. 6.9e-21;
 Matches 78; Conservative 24; Mismatches 70; Indels 23; Gaps 3;

 QY 10 GHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISAFSHVNIKL 69
 DB 10 GLFPRMLWALLLLAASLNAYNHVMDKPCCTEHEVSVNRGSRVVMACNISNLRDVTIELV 69

 QY 70 AHGQESAINEVAPGVSRDQWQLOVQGVQALVIKGDARDSHAGLYMHLVGHQNNRQV 129
 DB 70 TSEKTSIIFNQTPGNTSKOSQWUHQGGQALVITDAQKHSGEYWKURGLQAEFKNF 129

 QY 130 TLEVSGAEPQAPDTPGFVPV-----AVVTAVFILLVA-----LVMFAYRCRCQQ 177
 DB 130 NLIVNAADRKQTEDLPTVKPDKSTAVTEVIIATIIITIGVFWY-----181

 QY 178 REKKFPLEPQMKVA 192
 DB 182 ---KQFPVAPQIQMS 193

 RESULT 6
 SCTM_MOUSE STANDARD; PRT; 212 AA.
 AC Q9JL59;
 ID 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Secreted and transmembrane protein 1 precursor.
 GN Name=Sectm1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND INTERACTION WITH CD7.
 RC TISSUE=Colon;
 RX MEDLINE=20119303; PubMed=10652336; DOI=10.1074/jbc.275.5.3431;
 RA Lyman S.D., Escobar S., Rouseau A.-M., Armstrong A., Fanslow W.C.;
 RT "Identification of CD7 as a cognate of the human K12 (SECTM1)
 RL protein.";
 RL J. Biol. Chem. 275:3431-3437(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marasina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBUNIT: Interacts with CD7.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable). Also
 CC found as secreted (By similarity).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF210700; AAF30406.1; -;
 DR EMBL; BC010805; AAH10805.1; -;
 DR MGD; MGI:1929083; Sectm1.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR SMART; SM00409; IG; 1;
 KW SIGNAL; Transmembrane.
 FT CHAIN 1 28 Potential.
 FT 29 212 Secreted and transmembrane protein 1.
 FT DOMAIN 29 160 Extracellular (Potential).
 FT TRANSMEM 161 181 Potential.
 FT DOMAIN 182 212 Cytoplasmic (Potential).
 FT DISULFID 38 55 Potential.
 FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 85 85 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 130 130 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 212 AA; 23477 MW; 75113E877A2C5B87 CRC64;

 Query Match 24.9%; Score 326; DB 1; Length 212;
 Best Local Similarity 37.8%; Pred. No. 9.4e-21;
 Matches 74; Conservative 25; Mismatches 73; Indels 24; Gaps 2;

 QY 10 GHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISAFSHVNIKL 69
 DB 10 GLFPRMLWALLLLAASLNAYNHVMDKPCCTEHEVSVNRGSRVVMACNISNLRDVTIELV 69

 QY 70 AHGQESAINEVAPGVSRDQWQLOVQGVQALVIKGDARDSHAGLYMHLVGHQNNRQV 129
 DB 70 TSEKTSIIFNQTPGNTSKOSQWUHQGGQALVITDAQKHSGEYWKURGLQAEFKNF 129

 QY 130 TLEVSGAEPQAPDTPGFVPV-----AVVTAVFILLVA-----LVMFAYRCRCQQ 176
 DB 130 NLIVNAADRKQTEDLPTVKPDKSTAVTEVIIATIIITIGVFWY-----182

 QY 177 REKKFPLEPQMKVA 192
 DB 183 ---KQFPVAPQIQMS 194

 RESULT 7
 Q9D966 PRELIMINARY; PRT; 212 AA.
 ID Q9D966
 AC Q9D966;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
 DE library, clone:181003C24 product:secreted and transmembrane 1, full
 DE insert sequence.
 GN Name=Sectm1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.


```
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Skin;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki T., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tonaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK029082; BAC26284.1; -.
DR MGD; MGI:1929083; Sectm1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR SMART; SM00409; IG; 1.
KW Transmembrane.
SQ SEQUENCE 212 AA; 23559 MW; C863064DCE36EB7E CRC64;
Query Match 24.8%; Score 324; DB 2; Length 212;
Best Local Similarity 37.8%; Pred. No. 1.4e-20;
Matches 74; Conservative 25; Mismatches 73; Indels 24; Gaps 2;
Qy 10 GHVSQAQLTLFLAASLSAQNEGDSPTCTEGVSVSGENTVMSCNISNAFVHNKLR 69
Db 10 GLFPRMLWALLLAASLNAYNHVNDKPCCTEHEVSVNRGSRVVMACNLSNNLRDVTIELV 69
Qy 70 AHGESAIFNEVAPGYFSDRWQLOVQGGVAQLVIKGRDASHAGLVHMLVGHORNROV 129
Db 70 TSKTSTSIIFNTPFGNYSKDSQWLHIQGGQALVITDAQGHKSGEYWMKLRGFOAEFKNF 129
Qy 130 TLEVSGAEPOSAPDPTGFVPV-----AVTAVFILLVALVMPFAMWYRCRCSQ 176
Db 130 NLIWNAORQKTEDLPVTKVDPKPTAVRTEVIIIAITIIITIGTVGFVWY----- 182
Qy 177 RREKKFFLEPQMKVA 192
Db 183 ----KQPPVAPQIQMS 194
RESULT 9
ID Q52289 PRELIMINARY; PRT; 550 AA.
AC Q52289;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE UxPA protein.
GN Name=uxpA;
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WCS358;
RX MEDLINE=9618681; PubMed=8602167; DOI=10.1007/s004380050102;
RA de Groot A., Krizger J.J., Filloux A., Tomassen J.;
RT "Characterization of type II protein secretion (xcp) genes in the
RT plant growth-stimulating Pseudomonas putida, strain WCS358.";
RL Mol. Gen. Genet. 250:491-504(1996).
RN [2]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=WCS358;
RA de Groot A.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; X81085; CAA56977.1; -.
DR PIR; S64725; S64725.
SQ SEQUENCE 550 AA; 59118 MW; 684D79D0D279868B CRC64;
Query Match 7.9%; Score 103.5; DB 2; Length 550;
Best Local Similarity 23.2%; Pred. No. 1.4;
Matches 72; Conservative 42; Mismatches 118; Indels 79; Gaps 16;
Qy 2 QTCLAPPGHVSOA-LGTLFLFAA-----SLSAQN-EGWDSPTCTEGVSVS 46
Db 90 QLAPLLDAGRADEANLGGYAVLALLLEQLGEGAGAGNSLTLENGQGWNG-----SGLAYLT 145
Qy 47 WGMTVMSCNISNAFVHNKLR--HGQSAIFNEVAPGYFSR-----DWQ 92
Db 146 QGSEGVQSGQLLSEARVSDERVLWQPSAALYRQASATTLGLAGLADEQRQALGLEPLQ 205
Qy 93 LQVOGGVAQLVIK-----ARDSHAGLVHMLVGHORNROVTLVSGAEPOSAP-- 142
Db 206 LFERGG-ARIAVVGVTDPVAQDQKASLKQWYQALLPVFOQARREADLVVALADVTGPG 264
Qy 143 -----DTGFVPVPAVVTAVFILLVALVMPFAM-----YRCRC---SQ 176
Db 265 WLAERLPATDLLLCARGQDLWPTFVQATQASGRVP-VLPAGCRGSGAFRLRCQVAGOW 323
Qy 177 RREKKFF-----LLEPQMKVAALRAGAQGLSASAEELWTPDSEPTPR-PLALVFKPSPL 230
Db 324 QFSGFRFPTEQTLSPAAQVRAGLOALNQQRAGHAAML--DOPLARAPQALWRRDTRG 381
Qy 231 GALELSLPQPL 241
Db 382 GSWDRLLHQAL 392
RESULT 10
ID SHS1_BOVIN STANDARD; PRT; 506 AA.
AC O46631; O46632;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE (SHP substrate-1) (SHPS-1) (inhibitory receptor SHPS-1) (Signal-
DE regulatory protein alpha-1) (SIRP-alpha-1) (MyD-1 antigen).
GN Name=PTNS1; Synonyms=MYD1, SHPS1, SIRP;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS SBR-23; ALA-28; LEU-61; ARG-70;
RP HIS-120; 125-GLN; 127-GLY; 129-HIS; 132-VAL; ASN-145; VAL-153;
RP ASP-203; ARG-261; LEU-302; LEU-316; ARG-337; ASN-367; LEU-422; PHE-429
RP AND GLU-433.
RC STRAIN=Friesian; TISSUE=Peripheral blood;
RX MEDLINE=98143722; PubMed=9485180;
RX DOI=10.1002/(SICI)1521-4141(199801)28:01<1::AID-IMMU1>3.3.CO;2-M;
RA Brooke G.P., Parsons K.R., Howard C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells.";
RL Eur. J. Immunol. 28:1-11(1998).
CC -I- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC as docking protein and induces translocation of PTPN6, PTPN11 and
CC other binding partners from the cytosol to the plasma membrane.
CC Supports adhesion of cerebellar neurons, neurite outgrowth and
CC glial cell attachment. May play a key role in intracellular
CC signaling during synaptogenesis and in synaptic function. Involved
CC in the negative regulation of receptor tyrosine kinase-coupled
```



```
Db 348 ----VCERDDHTSAQLTVSVPRVVKFMSGLSTVVAEBGEATFCQVSPSDVAVV----- 399
Qy 166 FAWYRCRCQQREKKFFLLEPQMKVAALRAGAQQGLSRASAE-----WTPDSPTPRP 220
Db 400 --WFRDGA-----LLQSEKFAISQSGASHLSLISDLVLEDAQGITVBAEGASS 447
Qy 221 LALVFKPSPGLGALELLSPQ 239
Db 448 AALRVREAPVLFKKLEFQ 466

RESULT 14
Q9V5F7 PRELIMINARY; PRT; 894 AA.
AC Q9V5F7;
DT 01-MAY-2000 (Tremblrel. 12, Created)
DT 01-OCT-2002 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CG2292-PA.
GN ORFNames=CG2292;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN RP
SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Besson K.Y., Benos P.V., Berland B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
Fowler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck M.,
Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Stong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster."
Science 287:2185-2195 (2000).
[2]
SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
```

```
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
[3]
SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
[4]
SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
[5]
SEQUENCE FROM N.A.
FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AE003831; AAF58853.2;
DR FlyBase; FBgn0033479; CG2292.
DR InterPro; IPR007070; PIGN.
DR Pfam; PF04987; PIGN; 1.
SQ SEQUENCE 894 AA; 101828 MW; 9BD68206E9595187 CRC64;

Query Match 7.4%; Score 97; DB 2; Length 894;
Best Local Similarity 22.7%; Pred. No. 8.8;
Matches 62; Conservative 33; Mismatches 88; Indels 90; Gaps 15;

Qy 9 PGHVSQALGTLLFLAASLSAQNEGWDS-PICTEGWSVS-----WGENTVMSNCISNAFS 62
Db 95 PGHTLIAG-----LYEDPSAVLRGKSNPDI DFVFNRSQTYANGANDVL-----NVFS 145
Qy 63 HVN-----IKLRAHQESAI FNEVAPGY--FSRDGWLQVQGVQALVIKGARDSHAGLYM 116
Db 146 HVSNGGBINLRFYNHDL----DFSPGYDAYEEDSEWFKRVKLLQKQREALQRAQNVVFF 201
Qy 117 WHLVGHORNNQVTVLEYSV--AEQSPADTGFWPVAVVAVFILLVALVFWAVRCRCSQ 175
Db 202 LHLG-----LDTAGHVHKPGAP-----KFRRTL 225
Qy 176 QRREK-----KFFLEPQMKVAALRAGAQQGLSRASAE-----LW-TPDS 214
Db 226 EKTEKGVYVYQFERVFPDKRTAYLLT-ADHGWTDSGAHSGSPHETDTPFMLWGAGAS 284
Qy 215 EPTPRPALVFKPS-----PLGALELLSPOPL 241
Db 285 RAVPKPGCGTFMPNNEGPAAMPLELEQAQLTPL 317

RESULT 15
Q88F09 PRELIMINARY; PRT; 550 AA.
AC Q88P09;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
```

Search completed: October 17, 2005, 07:15:33
Job time : 127 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005. CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2005, 06:04:49 ; Search time 122 Seconds
(without alignments)
786.201 Million cell updates/sec

Title: US-10-080-522-1
Perfect score: 1308
Sequence: 1 MQTCLAPGCHVSQALGTLL.....PLGALLELLSPQLFPYAADP 248

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1308	100.0	248	2 AAW48811	Aaw48811 K12 prote
2	1308	100.0	248	2 AAY21846	Aay21846 Human sig
3	1308	100.0	248	4 AAB36658	Aab36658 Human K12
4	1308	100.0	248	8 ADJ75366	Adj75366 Marker ge
5	1308	100.0	248	8 ADP24664	Adp24664 PRO polyp
6	916.5	70.1	183	6 AAO29897	Aao29897 Human org
7	720.5	55.1	149	7 ADB36336	Adb36336 Human imm
8	719.5	55.0	162	6 AAO29896	Aao29896 Human org
9	492	37.6	101	6 AAO29895	Aao29895 Human org
10	326	24.9	212	4 AAB36660	Aab36660 Mouse K12
11	326	24.9	212	8 ADJ76167	Adj76167 Marker ge
12	325	24.8	212	8 ADJ76168	Adj76168 Marker ge
13	294	22.5	107	6 AAO29898	Aao29898 Human org
14	286	21.9	55	3 AAB34671	Aab34671 Gene 35 h
15	279	21.3	55	3 AAB34672	Aab34672 Human sec
16	163	12.5	30	3 AAB34673	Aab34673 Gene 35 h
17	156	11.9	43	7 ADB36337	Adb36337 Human imm
18	100	7.6	874	4 ABB59013	Abb59013 Drosoephil
19	96	7.3	435	6 ABR44273	Abr44273 Human DIT
20	96	7.3	442	4 AAB95569	Aab95569 Human pro
21	95.5	7.3	506	5 ADI16910	Adi16910 Cow NOVX
22	91	7.0	6620	7 ADJ70485	Adj70485 Human hea
23	91	7.0	7968	6 ABG76187	Abg76187 Human ser
24	90.5	6.9	1171	7 ABO63781	Abo63781 Klebstell
25	89	6.8	435	4 AAB61190	Aab61190 Mature hu

ALIGNMENTS

RESULT 1

AAW48811
ID AAW48811 standard; protein; 248 AA.

XX AAW48811;

AC AAW48811;

XX 26-OCT-1998 (first entry)

XX K12 protein.

DE K12 protein.

XX DNA probe; CD7 Hs1 DNase hypersensitive site; mRNA northern blot;

XX human erythroleukemic; HEL; K562 cell line; Clone; breast cancer;

XX ovarian cancer; malignant; tumour.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 239 /note= "encoded by CCAA"

XX WO9822502-A1.

XX 28-MAY-1998.

XX 24-NOV-1997; 97WO-US021517.

XX 22-NOV-1996; 96US-00755559.

XX (UYDU-) UNIV DUKE.

XX Kaufman RE, Slentz-Kesler KA;

XX WPI; 1998-312415/27.

XX N-PSDB; AAV32446.

XX New isolated K12 protein gene - which is over expressed in certain

XX neoplastic cells, used to develop products for tumour detection and

XX treatment.

XX Claim 3; Fig 1; 44pp; English.

XX This present sequence represents the K12 protein, the gene for which has

XX been located on chromosome 17q25. To obtain this genes cDNA sequence a

XX 500 bp DNA probe, which can be located just upstream of the CD7 Hs1 DNase

XX hypersensitive site, was used against a mRNA northern blot. From this a

XX 1.8kb transcript was detected in the human erythroleukemic cell line HEL.

XX The probe was then used to screen a human erythroleukemic cell line K562

XX cDNA library, from which several clones were identified and isolated that

Abo32633 Secreted
Adb90720 Human INT
Adf71455 Human INT
Aag10281 Human pol
Aab61188 Human INT
Abo32631 Secreted
Adb90718 Human INT
Adf71453 Human INT
Adn10279 Human pol
Adn99576 Novel hum
Abul5711 Protein e
Aar12427 Hybrid Pc
Abo79025 Pseudomon
Adg59388 Human can
Adq76631 Human but
Adq76633 Human but
Abm83615 Human dia
Adq67749 Novel hum
Abr58656 Human can
Abp69627 Human pol

CC constituted a 1.8kb cDNA. This cDNA was designated K12 and was found to
 CC have a single open reading frame as well as being in the same orientation
 CC as CD7. The K12 gene was found to be expressed in both breast and ovarian
 CC cancer cells at a much higher level than any other malignant or normal
 CC tissue that was examined, thus enabling the K12 to be a useful protein in
 CC tumour detection and treatment

XX SQ Sequence 248 AA;

Query Match 100.0%; Score 1308; DB 2; Length 248;
 Best Local Similarity 100.0%; Pred. No. 1.8e-133;
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTCTLAPFGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSNCISNA 60
 DB 1 MOTCTLAPFGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSNCISNA 60

QY 61 FSHVNIKLRAHGQESAIENEVAPGYFSRDGWLQVGGVAQLVIKARDSHAGLYMWHLV 120
 DB 61 FSHVNIKLRAHGQESAIENEVAPGYFSRDGWLQVGGVAQLVIKARDSHAGLYMWHLV 120

QY 121 GHQNNRQVTLVSGAEPQSPADTGFVPVAVTAVFILLVALVNFAYRCRCQORREK 180
 DB 121 GHQNNRQVTLVSGAEPQSPADTGFVPVAVTAVFILLVALVNFAYRCRCQORREK 180

QY 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPSETPRPLALVFKPSPGLALELLSPQ 240
 DB 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPSETPRPLALVFKPSPGLALELLSPQ 240

QY 241 LFPYAADP 248
 DB 241 LFPYAADP 248

RESULT 2

AAAY21846
 ID AAAY21846 standard; protein; 248 AA.

XX AC AAAY21846;

XX DT 20-SEP-1999 (first entry)

XX DE Human signal peptide-containing protein (SIGP) (clone ID 1747327).

XX KW Signal-peptide containing protein; SIGP; human; cancer; immune response;
 KW adenocarcinoma; leukemia; lymphoma; melanoma; myeloma; sarcoma; AIDS;
 KW Addison's disease; adult respiratory distress syndrome; allergy; anemia;
 KW asthma; atherosclerosis; bronchitis; cholecystitis; Crohn's disease;
 KW ulcerative colitis; atopic dermatitis; dermatomyositis; emphysema;
 KW diabetes mellitus; atrophic gastritis; glomerulonephritis; gout; trauma;
 KW Grave's Disease; hyperesinophilia; irritable bowel syndrome; infection;
 KW lupus erythematosus; multiple sclerosis; myasthenia gravis; inflammation;
 KW osteoarthritis; osteoporosis; pancreatitis; polymyositis; scleroderma;
 KW rheumatoid arthritis; Sjogren's syndrome; autoimmune thyroiditis.

XX OS Homo sapiens.

XX PN WO9933981-A2.

XX PD 08-JUL-1999.

XX PF 22-DEC-1998; 98WO-US027598.

XX PR 31-DEC-1997; 97US-00002485.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Lal P, Hillman JL, Corley NC, Guegler KJ, Baughn MR, Sather SK;
 XX PI Shah P;

XX DR WPI; 1999-430242/36.

XX DR N-PSDB; AA82061.

PT Human signal-peptide containing protein coding sequences used to treat
 XX cancer and immune responses.

XX PS Claim 1; Page 79-80; 99pp; English.

XX CC The invention provides human signal-peptide containing proteins (SIGP)
 CC (AA21841-855) and polynucleotides (AA82076-90) encoding the proteins. A
 CC host cell containing a vector comprising SIGP DNA can be used to produce
 CC the SIGP protein. The SIGP protein can be used, in conjunction with a
 CC pharmaceutical carrier to treat or prevent a cancer. An antagonist of the
 CC SIGP protein can be used to treat or prevent a cancer or an immune
 CC response. The cancers that can be treated or prevented include sarcomas,
 CC adenocarcinomas, leukemia's, lymphomas, melanomas, teratocarcinomas,
 CC myelomas and cancers of the adrenal gland, bladder, bone, bone marrow,
 CC brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract,
 CC heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis,
 CC prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and
 CC uterus. The immune responses that can be treated or prevented include
 CC AIDS, Addison's disease, adult respiratory distress syndrome, allergies,
 CC anemia, asthma, atherosclerosis, bronchitis, cholecystitis, Crohn's
 CC disease, ulcerative colitis, atopic dermatitis, dermatomyositis, diabetes
 CC mellitus, emphysema, atrophic gastritis, glomerulonephritis, Grave's
 CC disease, gout, hyperesinophilia, irritable bowel syndrome, lupus
 CC erythematosus, multiple sclerosis, myasthenia gravis, myocardial or
 CC pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis,
 CC polyomyositis, rheumatoid arthritis, scleroderma, Sjogren's syndrome, and
 CC autoimmune thyroiditis, complications of cancer, infections, and trauma

XX SQ Sequence 248 AA;

Query Match 100.0%; Score 1308; DB 2; Length 248;

Best Local Similarity 100.0%; Pred. No. 1.8e-133;

Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOTCTLAPFGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSNCISNA 60

DB 1 MOTCTLAPFGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSNCISNA 60

QY 61 FSHVNIKLRAHGQESAIENEVAPGYFSRDGWLQVGGVAQLVIKARDSHAGLYMWHLV 120

DB 61 FSHVNIKLRAHGQESAIENEVAPGYFSRDGWLQVGGVAQLVIKARDSHAGLYMWHLV 120

QY 121 GHQNNRQVTLVSGAEPQSPADTGFVPVAVTAVFILLVALVNFAYRCRCQORREK 180

DB 121 GHQNNRQVTLVSGAEPQSPADTGFVPVAVTAVFILLVALVNFAYRCRCQORREK 180

QY 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPSETPRPLALVFKPSPGLALELLSPQ 240

DB 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPSETPRPLALVFKPSPGLALELLSPQ 240

QY 241 LFPYAADP 248

DB 241 LFPYAADP 248

RESULT 3

AAB36658

ID AAB36658 standard; protein; 248 AA.

XX AC AAB36658;

XX DT 13-MAR-2001 (first entry)

XX DE Human K12 protein sequence SEQ ID NO:4.

XX KW Human; CD7; K12; cognate ligand; cluster of differentiation; cancer;
 KW identification; inhibiting T cell proliferation; HIV; infection;
 KW activating natural killer cell proliferation; leukaemia; lymphoma;
 KW sepsis; graft versus host disease; autoimmune disease; arthritis;
 KW multiple sclerosis; rheumatoid arthritis; psoriatic arthritis; lupus;
 KW scleroderma; psoriasis; atopic dermatitis; type I diabetes mellitus;
 KW Hashimoto's thyroiditis; pernicious anaemia; Addison's disease; uveitis;
 KW myasthenia gravis; psoriasis; Guillain-Barre Syndrome; Grave's disease;

systemic lupus erythematosus; dermatomyositis; asthma; eczema;
atopic dermatitis; contact dermatitis; eczematous dermatitis;
seborrheic dermatitis; rhinitis.

OS Homo sapiens.

XX WO20007333-A2.

XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014612.

XX 28-MAY-1999; 99US-0136450P.

XX (IMMUNEX CORP.

XX Lyman SD, Fanslow WC;

XX WPI; 2001-061511/07.

XX DR N-PSDB; AAC86152.

XX Stimulating intracellular signaling of CD7 comprises contacting a cell
expressing CD7 with recombinant K12 protein, the cognate ligand of CD7,
to inhibit T cell proliferation and/or activate natural killer cell
proliferation.

XX Claim 2; Page 38-39; 42pp; English.

XX The present invention describes a method for stimulating (S) the
intracellular signalling of CD (cluster of differentiation) 7 comprising
contacting a cell that expresses CD7 with a recombinant K12 protein (I),
the cognate ligand of CD7. (S) is useful for inhibiting T cell
proliferation and/or activating NK (natural killer) cell proliferation
and/or inducing NK toxicity in a mammal which involves administration of
K12 protein. It is also used for treating HIV-1 infection, cancer (T cell
leukemia, acute lymphocytic leukaemia, cutaneous T cell lymphoma),
bacterial and viral infections, mediated by CD7. In the case of treating
T cell leukemia the soluble K12 protein is covalently attached to a
toxin. A disease mediated by CD7 such as sepsis, graft versus host
disease due to transplantation, autoimmune diseases, multiple sclerosis,
arthritis, rheumatoid arthritis, psoriatic arthritis, scleroderma, lupus,
psoriasis, atopic dermatitis, type I diabetes mellitus, Hashimoto's
thyroiditis, pernicious anemia, Addison's disease, myasthenia gravis,
cervicitis, psoriasis, Guillain-Barre Syndrome, Grave's disease, systemic
lupus erythematosus and dermatomyositis, asthma, eczema, atopic
dermatitis, contact dermatitis, other eczematous dermatides, seborrheic
dermatitis, and rhinitis is also treated by administering a K12
antagonist (neutralising antibody). The present sequence represents the
human K12 protein, which is given in the exemplification of the present
invention

XX Sequence 248 AA;

Query March 100.08; Score 1308; DB 4; Length 248;
Best Local Similarity 100.08; Pred. No. 1.0e-133;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MOTCPAPFGHVSQALGTLFLFLASLSAQNGWDSPICTEGVSVSGWNTVMSCTNSNA 60
DB 1 MOTCPAPFGHVSQALGTLFLFLASLSAQNGWDSPICTEGVSVSGWNTVMSCTNSNA 60

OY 61 FSHVNIKLRAHQESAI FNEVAPGYFSRDGQVQGGVAQLVTKGARDSHAGLYMHLV 120
DB 61 FSHVNIKLRAHQESAI FNEVAPGYFSRDGQVQGGVAQLVTKGARDSHAGLYMHLV 120

OY 121 QHQRNRQVTLVSCAEPQSPADTGFWPVAWTAFTVILLVAFWYRCRCQQRREK 180
DB 121 QHQRNRQVTLVSCAEPQSPADTGFWPVAWTAFTVILLVAFWYRCRCQQRREK 180

OY 181 KFFLELPQMKVAALRAGAQOGLSRASAEIWPDPSETPRPLALVFKPSPLCALSLSPQ 240
DB 181 KFFLELPQMKVAALRAGAQOGLSRASAEIWPDPSETPRPLALVFKPSPLCALSLSPQ 240

OY 241 LFPYAADP 248
DB 241 LFPYAADP 248

RESULT 4
ADJ75366
ID ADJ75366 standard; protein; 248 AA.
XX AC ADJ75366;
XX 20-MAY-2004 (first entry)
XX Marker gene related amino acid sequence SEQ ID NO:618.
XX bronchial asthma; chronic obstructive pulmonary disease;
XX respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX gene therapy; marker.
XX Homo sapiens.
XX EPI394274-A2.
XX 03-MAR-2004.
XX 04-AUG-2003; 2003EP-00254857.
XX 06-AUG-2002; 2002JP-00229312.
XX 20-MAR-2003; 2003JP-00077212.
XX (GENO-) GENOX RES INC.
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;
XX WPI; 2004-193155/19.
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.

XX Example 11; SEQ ID NO 618; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (I) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (I) has respiratory
XX and antiasthmatic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.


```

XX SQ Sequence 149 AA;
Query Match 55.1%; Score 720.5; DB 7; Length 149;
Best Local Similarity 97.2%; Pred. No. 8e-70; Indels 1; Gaps 1;
Matches 138; Conservative 1; Mismatches 2;

Qy 1 MOTCPAPFGHVSQALGTLFLAASLSAQNEGWDSPTCTEGVSVSMGENTVMSNCISNA 60
Db 1 MOTCPAPFGHVSQALGTLFLAASLSAQNEGWDSPTCTEGVSVSMGENTVMSNCISNA 60
Qy 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGQLOVQGGVAQLVIKGARDSHAGLYMWHLV 120
Db 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGQLOVQGGVAQLVIKGARDSHAGLYMWHLV 120
Qy 121 GHQNNRQVTLVSGAE-PSNA 141
Db 121 GHQNNRQVTLVSGAAVPSNA 142

RESULT 8
AAO29896
ID AAO29896 standard; protein; 162 AA.
XX AAO29896;
XX 03-SEP-2003 (first entry)
XX Human organelle-associated protein (ORGA)-9.
XX Human; organelle-associated protein; ORGA; cell proliferative disorder;
KW actinic keratosis; arteriosclerosis; reproductive disorder; infertility;
KW endometriosis; gastrointestinal disorder; ectopic pregnancy; hepatitis;
KW gastroenteritis; neurological disorder; Alzheimer's disease; cirrhosis;
KW glomerulonephritis; renal amyloidosis; renal failure; Addison's disease;
KW renal disorder; ovulatory defect; teratogenesis; Pick's disease; cancer;
KW Huntington's disease; urologic disorder; cystitis; dementia; dysphagia;
KW indigestion; gastritis; hypertension; gene therapy; bursitis; anorexia;
KW infection; urethritis; prostatitis.
XX Homo sapiens.
XX WO2003044171-A2.
XX 30-MAY-2003.
XX 15-NOV-2002; 2002WO-US036807.
XX 16-NOV-2001; 2001US-0332384P.
XX 13-DEC-2001; 2001US-0341187P.
XX 23-JAN-2002; 2002US-0351151P.
XX 27-FEB-2002; 2002US-0360269P.
XX 05-APR-2002; 2002US-0370637P.
XX 14-JUN-2002; 2002US-0388946P.
XX (INCY-) INCYTE GENOMICS INC.
XX Ramkumar J, Burford N, Xu Y, Chawla NK, Kable AE, Becha SD;
XX Richardson TW, Gorvad AE, Sprague WW, Elliott VS, Khare R;
XX Hawkins PR, Jin P, Lee SY, Marquis JP, Swarnakar A, Wilson AD;
XX Hafalia AJA, Bulloch S;
XX WPI; 2003-457603/43.
XX N-PSDB; AAL60549.
XX New organelle-associated proteins and polynucleotides, useful for
PT diagnosing, treating and/or preventing cell proliferative, reproductive,
PT gastrointestinal, neurological, urologic, and renal disorders.
XX Claim 1; Page 166; 194pp; English.
XX PS
XX CC The invention relates to human organelle-associated proteins (ORGA) and
XX CC nucleic acid molecules encoding such proteins. ORGA sequences are useful

```

```

CC for diagnosing, treating and/or preventing cell proliferative disorders
CC (e.g. actinic keratosis, arteriosclerosis, bursitis, cirrhosis, cancers
CC or hepatitis), reproductive disorders (e.g. infertility, endometriosis,
CC ovulatory defects, ectopic pregnancy or teratogenesis), gastrointestinal
CC disorders (e.g. dysphagia, peptide oesophagitis, gastritis, indigestion,
CC anorexia or gastroenteritis), neurological disorders (e.g. Alzheimer's
CC disease, Pick's disease, Huntington's disease or dementia), urologic
CC disorders (e.g. infection, urethritis, cystitis, prostatitis or upper
CC tract infections) and renal disorders (e.g. glomerulonephritis, renal
CC amyloidosis, renal failure, Addison's disease or hypertension). The
CC invention is also useful in gene therapy. The present sequence is human
CC ORGA protein
XX
SQ Sequence 162 AA;
Query Match 55.0%; Score 719.5; DB 6; Length 162;
Best Local Similarity 89.1%; Pred. No. 1.2e-69;
Matches 139; Conservative 0; Mismatches 6; Indels 11; Gaps 1;

Qy 1 MOTCPAPFGHVSQALGTLFLAASLSAQNEGWDSPTCTEGVSVSMGENTVMSNCISNA 60
Db 1 MOTCPAPFGHVSQALGTLFLAASLSAQNEGWDSPTCTEGVSVSMGENTVMSNCISNA 60
Qy 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGQLOVQGGVAQLVIKGARDSHAGLYMWHLV 120
Db 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGQLOVQGGVAQLVIKGARDSHAGLYMWHLV 120
Qy 121 GHQNNRQVTLVSGAE-PSAPDTG 145
Db 121 GHQNNRQVTLVSGEVLPPRTDGRSPGSGPAG 156

RESULT 9
AAO29895
ID AAO29895 standard; protein; 101 AA.
XX AAO29895;
XX 03-SEP-2003 (first entry)
XX Human organelle-associated protein (ORGA)-8.
XX Human; organelle-associated protein; ORGA; cell proliferative disorder;
KW actinic keratosis; arteriosclerosis; reproductive disorder; infertility;
KW endometriosis; gastrointestinal disorder; ectopic pregnancy; hepatitis;
KW gastroenteritis; neurological disorder; Alzheimer's disease; cirrhosis;
KW glomerulonephritis; renal amyloidosis; renal failure; Addison's disease;
KW renal disorder; ovulatory defect; teratogenesis; Pick's disease; cancer;
KW Huntington's disease; urologic disorder; cystitis; dementia; dysphagia;
KW indigestion; gastritis; hypertension; gene therapy; bursitis; anorexia;
KW infection; urethritis; prostatitis.
XX Homo sapiens.
XX WO2003044171-A2.
XX 30-MAY-2003.
XX 15-NOV-2002; 2002WO-US036807.
XX 16-NOV-2001; 2001US-0332384P.
XX 13-DEC-2001; 2001US-0341187P.
XX 23-JAN-2002; 2002US-0351151P.
XX 27-FEB-2002; 2002US-0360269P.
XX 05-APR-2002; 2002US-0370637P.
XX 14-JUN-2002; 2002US-0388946P.
XX (INCY-) INCYTE GENOMICS INC.
XX Ramkumar J, Burford N, Xu Y, Chawla NK, Kable AE, Becha SD;
XX Richardson TW, Gorvad AE, Sprague WW, Elliott VS, Khare R;
XX Hawkins PR, Jin P, Lee SY, Marquis JP, Swarnakar A, Wilson AD;
XX Hafalia AJA, Bulloch S;

```

XX DR WPI; 2003-457603/43.
 XX DR N-PSDB; AAL60548.
 XX PT New organelle-associated proteins and polynucleotides, useful for
 XX PT diagnosing, treating and/or preventing cell proliferative, reproductive,
 XX PT gastrointestinal, neurological, urologic, and renal disorders.
 XX PS Claim 1; Page 165-166; 194pp; English.
 XX CC The invention relates to human organelle-associated proteins (ORGA) and
 CC nucleic acid molecules encoding such proteins. ORGA sequences are useful
 CC for diagnosing, treating and/or preventing cell proliferative disorders
 CC (e.g. actinic keratosis, arteriosclerosis, buritis, cirrhosis, cancers
 CC or hepatitis), reproductive disorders (e.g. infertility, endometriosis,
 CC ovulatory defects, ectopic pregnancy or teratogenesis), gastrointestinal
 CC disorders (e.g. dysphagia, peptide oesophagitis, gastritis, indigestion,
 CC anorexia or gastroenteritis), neurological disorders (e.g. Alzheimer's
 CC disease, Pick's disease, Huntington's disease or dementia), urologic
 CC disorders (e.g. infection, urethritis, cystitis, prostatitis or upper
 CC tract infections) and renal disorders (e.g. glomerulonephritis, renal
 CC amyloidosis, renal failure, Addison's disease or hypertension). The
 CC invention is also useful in gene therapy. The present sequence is human
 CC ORGA protein
 XX CC
 XX SQ Sequence 101 AA;
 Query Match 37.6%; Score 492; DB 6; Length 101;
 Best Local Similarity 100.0%; Pred. No. 3.5e-45;
 Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MOTCLAPPGHVQSALGTLFLAASLSAQNGWDSPICTEGVSVSGWNTVMSCNTSNA 60
 Db 1 MOTCLAPPGHVQSALGTLFLAASLSAQNGWDSPICTEGVSVSGWNTVMSCNTSNA 60
 Qy 61 FSHVNIKLRAHQESAIENEVAPGYFSRDGQ 92
 Db 61 FSHVNIKLRAHQESAIENEVAPGYFSRDGQ 92
 RESULT 10
 AAB36660
 ID AAB36660 standard; protein; 212 AA.
 XX AC AAB36660;
 XX DT 13-MAR-2001 (first entry)
 XX DE Mouse K12 protein sequence SEQ ID NO:8.
 XX KW Mouse; CD7; K12; cognate ligand; cluster of differentiation; cancer;
 KW identification; inhibiting T cell proliferation; HIV; infection;
 KW activating natural killer cell proliferation; leukaemia; lymphoma;
 KW sepsis; graft versus host disease; autoimmune disease; arthritis;
 KW multiple sclerosis; rheumatoid arthritis; psoriatic arthritis; lupus;
 KW scleroderma; psoriasis; atopic dermatitis; type 1 diabetes mellitus;
 KW Hashimoto's thyroiditis; pernicious anaemia; Addison's disease; uveitis;
 KW myasthenia gravis; psoriasis; Guillain-Barre Syndrome; Grave's disease;
 KW systemic lupus erythematosus; dermatomyositis; asthma; eczema;
 KW atopic dermatitis; contact dermatitis; eczematous dermatitis;
 KW seborrheic dermatitis; rhinitis.
 XX OS Mus sp.
 XX PN WO200073333-A2.
 XX XX
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US014612.
 XX PR 28-MAY-1999; 99US-0136450P.
 XX PR (IMMV) IMMUNEX CORP.
 XX FA

XX Lyman SD, Fanslow WC;
 XX WPI; 2001-061511/07.
 XX DR N-PSDB; AAC88154.
 XX PT Stimulating intracellular signaling of CD7 comprises contacting a cell
 XX PT expressing CD7 with recombinant K12 protein, the cognate ligand of CD7,
 XX PT to inhibit T cell proliferation and/or activate natural killer cell
 XX PT proliferation.
 XX PS Claim 32; Page 42; 42pp; English.
 XX CC The present invention describes a method for stimulating (S) the
 CC intracellular signalling of CD (cluster of differentiation) 7 comprising
 CC contacting a cell that expresses CD7 with a recombinant K12 protein (I),
 CC the cognate ligand of CD7. (S) is useful for inhibiting T cell
 CC proliferation and/or activating NK (natural killer) cell proliferation
 CC and/or inducing NK toxicity in a mammal which involves administration of
 CC K12 protein. It is also used for treating HIV-1 infection, cancer (T cell
 CC leukaemia, acute lymphocytic leukaemia, cutaneous T cell lymphoma),
 CC bacterial and viral infections, mediated by CD7. In the case of treating
 CC T cell leukaemia the soluble K12 protein is covalently attached to a
 CC toxin. A disease mediated by CD7 such as sepsis, graft versus host
 CC disease due to transplantation, autoimmune diseases, multiple sclerosis,
 CC arthritis, rheumatoid arthritis, psoriatic arthritis, scleroderma, lupus,
 CC psoriasis, atopic dermatitis, type 1 diabetes mellitus, Hashimoto's
 CC thyroiditis, pernicious anaemia, Addison's disease, myasthenia gravis,
 CC uveitis, psoriasis, Guillain-Barre Syndrome, Grave's disease, systemic
 CC lupus erythematosus and dermatomyositis, asthma, eczema, atypical
 CC dermatitis, contact dermatitis, other eczematous dermatides, seborrheic
 CC dermatitis, and rhinitis is also treated by administering a K12
 CC antagonist (neutralising antibody). The present sequence represents the
 CC mouse K12 protein, which is given in the exemplification of the present
 CC invention
 XX CC
 XX SQ Sequence 212 AA;
 Query Match 24.9%; Score 326; DB 4; Length 212;
 Best Local Similarity 37.8%; Pred. No. 1.2e-26;
 Matches 74; Conservative 25; Mismatches 73; Indels 24; Gaps 2;
 Qy 10 GHVSQALGTLFLAASLSAQNGWDSPICTEGVSVSGWNTVMSCNTSNAFHVNIKL 69
 Db 10 GLFPRMLWALLLAASLSAHNDVWDEPCCTEHEVSVNRGSRVNVACISNNLRDVTTLV 69
 Qy 70 AHGOESAIENEVAPGYFSRDGQQLVQGVQALVIKGDASHAGLYMMHLYGHQNRNQV 129
 Db 70 TSEKTSIIFNHTPPGNYKSDSWQLHIQGVQALVITDAQKHSGNSYKWLHGFQAEKNF 129
 Qy 130 TLEVSAGBSPASDPTGFWVP-----AVTAVFILLVALVMFAWYRCRSQQ 176
 Db 130 NLTVNAADROKTDLPVTKVPDPKPPTAVRTEVIIIAITTIITIGVFWY----- 182
 Qy 177 RREKKFPLEPOMKVA 192
 Db 183 -----KOPPVAPQIQMS 194
 RESULT 11
 ADJ76167
 ID ADJ76167 standard; protein; 212 AA.
 XX AC ADJ76167;
 XX XX
 XX DT 20-MAY-2004 (first entry)
 XX DE Marker gene related amino acid sequence SEQ ID NO:1419.
 XX KW bronchial asthma; chronic obstructive pulmonary disease;
 XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 XX KW gene therapy; marker.
 XX KW


```
Query Match      24.8%; Score 325; DB 8; Length 212;
Best Local Similarity 37.8%; Pred. NO. 1.5e-26;
Matches 74; Conservative 25; Mismatches 73; Indels 24; Gaps 2;

QY 10 GHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSGWNTVMSCNISNAFSHVNIKL 69
DB 10 GUPRMLWALLGLAASLAINVHWDKPCCTEHEVSVNRGSRVYVMAACNISNLRDTIELV 69
QY 70 AHGQSAIFNEVAPGFRDQWQLOVQGGVAQLVIKIGARDSHAGLYMHLVGHQRNNROV 129
DB 70 TSKKTSIFNQTPPGNYSKDSQLHIQGGQALVITDAQGHSGYWKLRGFQAEFNK 129
QY 130 TLEVSQASQSDAPDGFVFPV-----AVTAVFLLVALVNFAYRCRCRCSQQ 176
DB 130 NLIVNAADRQKTEDLPVTKVPDKPTAVRTEVIIIIATIIITIGIGVFVWY----- 182
QY 177 REKKFFLEPOMKVA 192
DB 183 ----KQFPVAPQIQMS 194

RESULT 13
ID AAO29898 standard; protein; 107 AA.
XX AAO29898;
AC
AD
DT 03-SEP-2003 (first entry)
DE Human organelle-associated protein (ORGA)-11.
XX
KW Human; organelle-associated protein; ORGA; cell proliferative disorder;
KW actinic keratosis; arteriosclerosis; reproductive disorder; infertility;
KW endometriosis; gastrointestinal disorder; ectopic pregnancy; hepatitis;
KW gastroenteritis; neurological disorder; Alzheimer's disease; cirrhosis;
KW glomerulonephritis; renal amyloidosis; renal failure; Addison's disease;
KW renal disorder; ovulatory defect; teratogenesis; Pick's disease; cancer;
KW Huntington's disease; urologic disorder; cystitis; dementia; dysphagia;
KW indigestion; gastritis; hypertension; gene therapy; bursitis; anorexia;
KW infection; urethritis; prostatitis.
XX
OS Homo sapiens.
XX
PN WO2003044171-A2.
XX
PD 30-MAY-2003.
XX
PF 15-NOV-2002; 2002WO-US036807.
XX
PR 16-NOV-2001; 2001US-0332384P.
PR 13-DEC-2001; 2001US-0341187P.
PR 23-JAN-2002; 2002US-0351151P.
PR 27-FEB-2002; 2002US-0360269P.
PR 05-APR-2002; 2002US-0370637P.
PR 14-JUN-2002; 2002US-0388946P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Ramkumar J, Burford N, Xu Y, Chawla NK, Kable AE, Becha SD;
PI Richardson TW, Gorvad AE, Sprague WW, Elliott VS, Khare R;
PI Hawkins PR, Jin P, Lee SY, Marquis JP, Swarnakar A, Wilson AD;
PI Hafalia AJA, Bulloch S;
XX
DR WPI; 2003-457603/43.
DR N-PSDB; AAL60551.
XX
PT New organelle-associated proteins and polynucleotides, useful for
PT diagnosing, treating and/or preventing cell proliferative, reproductive,
PT gastrointestinal, neurological, urologic, and renal disorders.
XX
PS Claim 1; Page 167; 194pp; English.
XX
```

```
CC The invention relates to human organelle-associated proteins (ORGA) and
CC nucleic acid molecules encoding such proteins. ORGA sequences are useful
CC for diagnosing, treating and/or preventing cell proliferative disorders
CC (e.g. actinic keratosis, arteriosclerosis, bursitis, cirrhosis, cancers
CC or hepatitis), reproductive disorders (e.g. infertility, endometriosis,
CC ovulatory defects, ectopic pregnancy or teratogenesis), gastrointestinal
CC disorders (e.g. dysphagia, peptide esophagitis, gastritis, indigestion,
CC anorexia or gastroenteritis), neurological disorders (e.g. Alzheimer's
CC disease, Pick's disease, Huntington's disease or dementia), urologic
CC disorders (e.g. infection, urethritis, cystitis, prostatitis or upper
CC tract infections) and renal disorders (e.g. glomerulonephritis, renal
CC amyloidosis, renal failure, Addison's disease or hypertension). The
CC invention is also useful in gene therapy. The present sequence is human
CC ORGA protein
XX
SQ Sequence 107 AA;

Query Match      22.5%; Score 294; DB 6; Length 107;
Best Local Similarity 100.0%; Pred. NO. 1.4e-23;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQTCPLAFPGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSGWNTVMS 55
DB 1 MQTCPLAFPGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSGWNTVMS 55

RESULT 14
ID AAB34671 standard; protein; 55 AA.
XX AAB34671;
AC AAB34671;
AD
DT 26-JAN-2001 (first entry)
DE Gene 35 human secreted protein homologous amino acid sequence #155.
XX
KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
KW antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic;
KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
KW hyperproliferative disorder; cancer; cardiovascular disorder; infection;
KW cerebrovascular disorder; angiogenesis; nervous system disorder;
KW ocular disorder; wound healing; skin aging; food additive; preservative.
XX
OS Homo sapiens.
XX
PN WO200056751-A1.
XX
PD 28-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006013.
XX
PR 19-MAR-1999; 99US-0125360P.
PR 11-JUN-1999; 99US-0138626P.
PR 03-DEC-1999; 99US-0168662P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-579482/54.
XX
PT Isolated nucleic acid molecule encoding a human secreted protein is used
PT in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 412; 419pp; English.
XX
CC The polynucleotide sequences given in AAC59738 to AAC59787 encode the
CC human secreted proteins given in AAB34577 to AAB34626. AAB34627 to
CC AAB34686 represent human secreted polypeptide sequences and proteins
CC homologous to them, which are given in the exemplification of the present
CC invention. Human secreted proteins have activities based on the tissues
CC and cells the genes are expressed in. Example of activities include:
CC
```


CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
 CC cytosatic; cardiant; vasotropic; cerebroprotective; nontropic;
 CC neuroprotective; antibacterial; virucide; fungicide; and
 CC ophthalmological. The polynucleotides and proteins can be used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms and
 CC cancers of the breast or liver, cardiovascular disorders, cerebrovascular
 CC disorders, angiogenesis, nervous system disorders, infections caused by
 CC bacteria, viruses and fungi and ocular disorders. The proteins can also
 CC be used to aid wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The proteins can also be used as a
 CC food additive or preservative to increase or decrease storage
 CC capabilities. AAC59729 to AAC59737 and AAB34576 represent sequences used
 CC in the exemplification of the present invention

XX SQ Sequence 55 AA;

Query Match 21.9%; Score 286; DB 3; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.9e-23;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 194 LRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALLELLSPQLFPYAADP 248

Db 1 LRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALLELLSPQLFPYAADP 55

RESULT 15

AAB34672

ID AAB34672 standard; protein; 55 AA.

XX AC AAB34672;

XX DT 26-JAN-2001 (first entry)

XX DE Human secreted protein sequence encoded by gene 35 SEQ ID NO:156.

XX KW Human; secreted protein; diagnosis; immunosuppressive; antirheumatic;
 KW antirheumatic; antiproliferative; cytosatic; cardiant; vasotropic;
 KW cerebroprotective; nontropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; neoplasm;
 KW hyperproliferative disorder; cancer; cardiovascular disorder; infection;
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;
 KW ocular disorder; wound healing; skin aging; food additive; preservative.

XX OS Homo sapiens.

XX OS WO200056751-A1.

XX PN 28-SEP-2000.

XX PD 09-MAR-2000; 2000WO-US006013.

XX PR 19-MAR-1999; 99US-0125360P.

XX PR 11-JUN-1999; 99US-0138626P.

XX PR 03-DEC-1999; 99US-0168662P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX XX Rosen CA, Ruben SM, Komatsoulis G;

XX XX WPI; 2000-579482/54.

XX XX Isolated nucleic acid molecule encoding a human secreted protein is used
 PT in preventing, treating or ameliorating a medical condition.

XX PS Disclosure; Page 412-413; 419pp; English.

XX CC The polynucleotide sequences given in AAC59738 to AAC59787 encode the

CC human secreted proteins given in AAB34577 to AAB34626. AAB34627 to
 CC AAB34686 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Example of activities include:
 CC antiarthritic; immunosuppressive; antirheumatic; antiproliferative;
 CC cytosatic; cardiant; vasotropic; cerebroprotective; nontropic;
 CC neuroprotective; antibacterial; virucide; fungicide; and
 CC ophthalmological. The polynucleotides and proteins can be used to
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
 CC in diagnosing a pathological condition or susceptibility to a
 CC pathological condition. Disorders which are diagnosed or treated include
 CC autoimmune diseases, hyperproliferative disorders e.g. neoplasms and
 CC cancers of the breast or liver, cardiovascular disorders, cerebrovascular
 CC disorders, angiogenesis, nervous system disorders, infections caused by
 CC bacteria, viruses and fungi and ocular disorders. The proteins can also
 CC be used to aid wound healing and epithelial cell proliferation, to
 CC prevent skin aging due to sunburn, to maintain organs before
 CC transplantation, for supporting cell culture of primary tissues, to
 CC regenerate tissues and in chemotaxis. The proteins can also be used as a
 CC food additive or preservative to increase or decrease storage
 CC capabilities. AAC59729 to AAC59737 and AAB34576 represent sequences used
 CC in the exemplification of the present invention

XX SQ Sequence 55 AA;

Query Match 21.3%; Score 279; DB 3; Length 55;

Best Local Similarity 98.2%; Pred. No. 2.3e-22;

Matches 54; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 194 LRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALLELLSPQLFPYAADP 248

Db 1 LRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALLELLSPQLFPYAADP 55

Search completed: October 17, 2005, 07:12:16

Job time : 127 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2005, 07:12:25 ; Search time 2066 Seconds
(without alignments)
50.036 Million cell updates/sec

Title: US-10-080-522-1

Perfect score: 1308

Sequence: 1 MOTCLPAPGHVSQALGTL.....PLGALELLSPQLFPFYADP 248

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1308	100.0	248	9	US-09-799-777-32 Sequence 32, Appl
2	1308	100.0	248	9	US-09-997-165-4 Sequence 4, Appli
3	1308	100.0	248	14	US-10-080-522-1 Sequence 1, Appli
4	1308	100.0	248	18	US-10-631-467-618 Sequence 618, App
5	326	24.9	212	9	US-09-997-165-8 Sequence 8, Appli
6	326	24.9	212	18	US-10-631-467-1419 Sequence 1419, Ap
7	325	24.8	212	18	US-10-631-467-1420 Sequence 1420, Ap
8	100	7.6	874	20	US-11-097-143-3831 Sequence 3831, Ap
9	98	7.5	969	15	US-10-052-648A-35 Sequence 35, Appl
10	96	7.3	969	15	US-10-052-648A-34 Sequence 34, Appl
11	95.5	7.3	506	15	US-10-072-012-446 Sequence 446, App

12	91.5	7.0	541	16	US-10-719-993-534	Sequence 534, App
13	91.5	7.0	597	15	US-10-425-114-62807	Sequence 62807, A
14	91.5	7.0	597	16	US-10-425-115-279214	Sequence 279214,
15	91	7.0	6620	15	US-10-080-334-290	Sequence 290, App
16	91	7.0	6620	16	US-10-408-765A-2291	Sequence 2291, Ap
17	91	7.0	7968	13	US-10-077-130-5	Sequence 5, Appli
18	89	6.8	435	10	US-09-759-130B-275	Sequence 275, App
19	89	6.8	435	14	US-10-189-123-5	Sequence 5, Appli
20	89	6.8	435	14	US-10-188-495-5	Sequence 5, Appli
21	89	6.8	435	16	US-10-741-790-275	Sequence 275, App
22	89	6.8	455	10	US-09-759-130B-273	Sequence 273, App
23	89	6.8	455	14	US-10-189-123-3	Sequence 3, Appli
24	89	6.8	455	14	US-10-188-495-3	Sequence 3, Appli
25	89	6.8	455	16	US-10-741-790-273	Sequence 273, App
26	84.5	6.5	271	14	US-10-156-761-14023	Sequence 14023, A
27	84.5	6.5	289	15	US-10-282-122A-43635	Sequence 43635, A
28	84.5	6.5	455	16	US-10-322-696-24	Sequence 24, Appli
29	84.5	6.5	455	16	US-10-742-682-2	Sequence 2, Appli
30	84.5	6.5	482	16	US-10-742-682-4	Sequence 4, Appli
31	84.5	6.5	567	18	US-10-737-318-8	Sequence 8, Appli
32	84.5	6.5	792	18	US-10-737-318-10	Sequence 10, Appl
33	84.5	6.5	829	18	US-10-737-318-12	Sequence 12, Appl
34	84.5	6.5	882	18	US-10-737-318-6	Sequence 6, Appli
35	83.5	6.4	199	14	US-10-095-131A-46	Sequence 46, Appl
36	83.5	6.4	199	14	US-10-095-131A-48	Sequence 48, Appl
37	83.5	6.4	366	14	US-10-091-438-153	Sequence 153, App
38	83.5	6.4	368	9	US-09-764-853-678	Sequence 19, Appl
39	83.5	6.4	468	17	US-10-626-832-19	Sequence 13729, A
40	83.5	6.4	699	15	US-10-369-493-13729	Sequence 311858,
41	83	6.3	340	16	US-10-425-115-311858	Sequence 107, App
42	82.5	6.3	286	16	US-10-367-094-107	Sequence 12, Appl
43	82.5	6.3	288	13	US-10-068-215-12	Sequence 12, Appl
44	82.5	6.3	288	14	US-10-115-615-12	Sequence 18, Appl
45	82.5	6.3	288	16	US-10-748-112-18	

ALIGNMENTS

RESULT 1

US-09-799-777-32

; Sequence 32, Application US/09799777

; Patent No. US20020091244A1

; GENERAL INFORMATION:

; APPLICANT: Lal, Preeti

; Hillman, Jennifer L.

; Corley, Neil C.

; Guegler, Karl J.

; Baugh, Mariah

; Sather, Susan

; Shah, Purvi

; TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS

; NUMBER OF SEQUENCES: 154

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,777

; FILING DATE: 06-Mar-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/002,485

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

```
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0459 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 32 :
US-09-799-777-32

Query Match 100.0%; Score 1308; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-124;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQTCLAPFGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
Db 1 MQTCLAPFGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60

Qy 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGHQLOVQGGVAQLVIKGARDSHAGLYMHWLV 120
Db 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGHQLOVQGGVAQLVIKGARDSHAGLYMHWLV 120

Qy 121 GHORNNROVTLVSGAEPOSAPDTGFVPVAVTAVFILLVALVWFAYRCRCQQORREK 180
Db 121 GHORNNROVTLVSGAEPOSAPDTGFVPVAVTAVFILLVALVWFAYRCRCQQORREK 180

Qy 121 GHORNNROVTLVSGAEPOSAPDTGFVPVAVTAVFILLVALVWFAYRCRCQQORREK 180
Db 121 GHORNNROVTLVSGAEPOSAPDTGFVPVAVTAVFILLVALVWFAYRCRCQQORREK 180

Qy 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQP 240
Db 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQP 240

Qy 241 LFPYAADP 248
Db 241 LFPYAADP 248

RESULT 2
US-09-997-165-4
; Sequence 4, Application US/09997165
; Patent No. US20020141999A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF
; FILE REFERENCE: 2913-US
; CURRENT APPLICATION NUMBER: US/09/997,165
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: PCT/US00/14612
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,450
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-997-165-4

Query Match 100.0%; Score 1308; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-124;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQTCLAPFGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
Db 1 MQTCLAPFGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60

Qy 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGHQLOVQGGVAQLVIKGARDSHAGLYMHWLV 120
Db 61 FSHVNIKLRAHGOESAIENEVAPGYFSRDGHQLOVQGGVAQLVIKGARDSHAGLYMHWLV 120

Qy 121 GHORNNROVTLVSGAEPOSAPDTGFVPVAVTAVFILLVALVWFAYRCRCQQORREK 180
Db 121 GHORNNROVTLVSGAEPOSAPDTGFVPVAVTAVFILLVALVWFAYRCRCQQORREK 180

Qy 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQP 240
Db 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQP 240

Qy 241 LFPYAADP 248
Db 241 LFPYAADP 248

RESULT 3
US-10-080-522-1
; Sequence 1, Application US/10080522
; Publication No. US20030096326A1
; GENERAL INFORMATION:
; APPLICANT: KAUFMAN, RUSSEL E.
; SLENTZ-KESLER, KIMBERLY
; TITLE OF INVENTION: GENE PRODUCT OVER EXPRESSED IN CANCER
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/080,522
; FILING DATE: 25-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/539,774
; FILING DATE: 31-MAR-2000
; APPLICATION NUMBER: US 09/210,474
; FILING DATE: 14-DEC-1998
; APPLICATION NUMBER: US 08/755,559
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-645
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-080-522-1

Query Match 100.0%; Score 1308; DB 14; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-124;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQTCLAPFGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
Db 1 MQTCLAPFGHVSOALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
```

Qy 61 FSHVNIKLRAHQESAIENEVAPGYFSRDGWLQVQGGVAQLVIKGARDSHAGLYMMHLV 120
Db 61 FSHVNIKLRAHQESAIENEVAPGYFSRDGWLQVQGGVAQLVIKGARDSHAGLYMMHLV 120
Qy 121 GHQRNNQVTLVSGAEQSPADTGFVPVPAVTVAVFILLVALVWFAYRCRCQORREK 180
Db 121 GHQRNNQVTLVSGAEQSPADTGFVPVPAVTVAVFILLVALVWFAYRCRCQORREK 180
Qy 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPDSEPTPRPLALVFKPSPLGALELLSPQ 240
Db 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPDSEPTPRPLALVFKPSPLGALELLSPQ 240
Qy 241 LFPYAADP 248
Db 241 LFPYAADP 248

RESULT 4

US-10-631-467-618
; Sequence 618, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genex Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631.467
; PRIOR FILING DATE: 2003-07-31
; PRIOR FILING DATE: 2003-07-31
; PRIOR FILING DATE: 2003-03-20
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 618
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-618

Query Match 100.0%; Score 1308; DB 18; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.9e-124;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MOTCPAPPGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
Db 1 MOTCPAPPGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
Qy 61 FSHVNIKLRAHQESAIENEVAPGYFSRDGWLQVQGGVAQLVIKGARDSHAGLYMMHLV 120
Db 61 FSHVNIKLRAHQESAIENEVAPGYFSRDGWLQVQGGVAQLVIKGARDSHAGLYMMHLV 120
Qy 121 GHQRNNQVTLVSGAEQSPADTGFVPVPAVTVAVFILLVALVWFAYRCRCQORREK 180
Db 121 GHQRNNQVTLVSGAEQSPADTGFVPVPAVTVAVFILLVALVWFAYRCRCQORREK 180
Qy 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPDSEPTPRPLALVFKPSPLGALELLSPQ 240
Db 181 KFFLLEPQMKVAALRAGAQQGLSRASAEIWTDPDSEPTPRPLALVFKPSPLGALELLSPQ 240
Qy 241 LFPYAADP 248
Db 241 LFPYAADP 248

RESULT 5

US-09-997-165-8
; Sequence 8, Application US/09997165
; Patent No. US20020141999A1
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Farslow, William C.
; TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF

; FILE REFERENCE: 2913-US
; CURRENT APPLICATION NUMBER: US/09/997.165
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: PCT/US00/14612
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,450
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-997-165-8

Query Match 24.9%; Score 326; DB 9; Length 212;
Best Local Similarity 37.8%; Pred. No. 1.4e-24;
Matches 74; Conservative 25; Mismatches 73; Indels 24; Gaps 2;
Qy 10 GHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNAFHVNIKL 69
Db 10 GLFPRMLWALLLAASLSNAHNDVMDPCCTEHEVSVNRSRVVMACNISNNLRDVTIELV 69
Qy 70 AHQGESAIENEVAPGYFSRDGWLQVQGGVAQLVIKGARDSHAGLYMMHLVGHQRNNQV 129
Db 70 TSEKTSIIFNHTPPGNYSKDSWOLHIQGVQVQVQVITDAQDKHSGNSWKLHGFQAEKFN 129
Qy 130 TLEVSGAEQSPADTGFVPV-----AVTVAVFILLVALVWFAYRCRCQ 176
Db 130 NLTVNAADROKTEDLPVTKVPDKPPTAVRTEVIIIIAIIATIIITIGIGVFWY----- 182
Qy 177 RREKKFFLEPQMKVA 192
Db 183 ----KQPPVAPQIQMS 194

RESULT 6

US-10-631-467-1419
; Sequence 1419, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genex Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive
; TITLE OF INVENTION: disease
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631.467
; CURRENT FILING DATE: 2003-07-31
; PRIOR FILING DATE: 2003-07-212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1419
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1419

Query Match 24.9%; Score 326; DB 18; Length 212;
Best Local Similarity 37.8%; Pred. No. 1.4e-24;
Matches 74; Conservative 25; Mismatches 73; Indels 24; Gaps 2;
Qy 10 GHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNAFHVNIKL 69
Db 10 GLFPRMLWALLLAASLSNAHNDVMDPCCTEHEVSVNRSRVVMACNISNNLRDVTIELV 69
Qy 70 AHQGESAIENEVAPGYFSRDGWLQVQGGVAQLVIKGARDSHAGLYMMHLVGHQRNNQV 129
Db 70 TSEKTSIIFNHTPPGNYSKDSWOLHIQGVQVQVQVITDAQDKHSGNSWKLHGFQAEKFN 129
Qy 130 TLEVSGAEQSPADTGFVPV-----AVTVAVFILLVALVWFAYRCRCQ 176

```

Db 130 NLTVNAADROKQEDLPVTKVPKDPPTAVRTEVIIIIAIIATIIITIGVFWY----- 182
Qy 177 RREKFFLLEPQMKVA 192
Db 183 ----KQFPVAPQIQMS 194

RESULT 7
US-10-631-467-1420
; Sequence 1420, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: Patencin version 3.1
; SEQ ID NO 1420
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1420

Query Match 24.8%; Score 325; DB 18; Length 212;
Best Local Similarity 37.8%; Pred. No. 1.8e-24;
Matches 74; Conservative 25; Mismatches 73; Indels 24; Gaps 2;

Qy 10 GHVSQALGTLFLAASLSAQNEGWDSPTCTGVSVSGENTVMSNINAFSHVNIKL 69
Db 10 GLFPRMLWALLAASLNAYNHVDKPCCTHEVSVNRGSRVMAACNINLRDVTIELV 69
Qy 70 AHGQSAIFNEVAPGYFGRDQVQGVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 129
Db 70 TSKKTSIIFNQTPPNYSKDSQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 129
Qy 130 TLEVSAGPQAPDPTGFVFPV-----AVTAVFILLVALVFMFAWYRCRCSQ 176
Db 130 NLIVNAADROKQEDLPVTKVPKDPPTAVRTEVIIIIAIIATIIITIGVFWY----- 182
Qy 177 RREKFFLLEPQMKVA 192
Db 183 ----KQFPVAPQIQMS 194

RESULT 8
US-11-097-143-3831
; Sequence 3831, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383

```

```

; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3831
; LENGTH: 874
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-3831

Query Match 7.6%; Score 100; DB 20; Length 874;
Best Local Similarity 23.2%; Pred. No. 0.98;
Matches 60; Conservative 33; Mismatches 84; Indels 82; Gaps 14;

Qy 9 PGHVSQALGTLFLAASLSAQNEGWDS-PICTEGVSVS-----WGENTVMSNINAFS 62
Db 95 PGHITLIAG---LYEDPSAVLRGKWSNPIDFDTVFNRSQTYAWGANDVL-----NVFS 145
Qy 63 HVN-----IKLRAHQBSAIFNEVAPGY--FSRDGWLQVQGVQVQVQVQVQVQVQV 116
Db 146 HVSNGEINLRFYNHDL-----DFSPGYDAYEEDWVFKRVKLLQKQKREALQRAQNVVFF 201
Qy 117 WHLVGHORNNRQVTVLEVSG-AEQSAPDPTGFVFPVAVTAVFILLVALVFMFAWYRCRCSQ 175
Db 202 LHLUG-----LDTAGHVHFGAP-----KFRRTL 225
Qy 176 QRREK-----KFFLLEPQMKVAALRAGAQGLSRASAEIWTDPSEPTPRPLALVFKPS 228
Db 226 EKTEKGVAIYQBFERFVDPKRTAYLLT-ADHGWTDSGA-----SRAVFKPGGRTFMPN 278
Qy 229 -----PLGALELLSQPL 241
Db 279 NEGPAFMLEHQALQTLPL 297

RESULT 9
US-10-052-648A-35
; Sequence 35, Application US/10052648A
; Publication No. US20040005538A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Burges, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Colman, Steven
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gunther, Erik
; APPLICANT: Kekuda, Ramesh
; APPLICANT: MacDougall, John R.
; APPLICANT: Mehraban, Fuad
; APPLICANT: Pothurajan, Meera
; APPLICANT: Rotherberg, Mark
; APPLICANT: Shimkets, Richard
; APPLICANT: Smithson, Glenda
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Stone, David J.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
; TITLE OF INVENTION: USING THE SAME
; FILE REFERENCE: 21402-250 (CURA-550)
; CURRENT APPLICATION NUMBER: US/10/052,648A
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/262,454
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/272,920
; PRIOR FILING DATE: 2001-03-02

```

```
/ PRIOR APPLICATION NUMBER: 60/284,549
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/303,229
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,605
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/269,098
/ PRIOR FILING DATE: 2001-02-15
/ PRIOR APPLICATION NUMBER: 60/264,159
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/271,855
/ PRIOR FILING DATE: 2001-02-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 97
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 35
/ LENGTH: 969
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: VARIANT
/ LOCATION: (848)..(889)
/ OTHER INFORMATION: Where Xaa is any amino acid
US-10-052-648A-35

Query Match          7.5%; Score 98; DB 15; Length 969;
Best Local Similarity 24.9%; Pred. No. 1.8;
Matches 51; Conservative 24; Mismatches 86; Indels 44; Gaps 10;

Qy  2 QTCPLAFPG----HVSQALGTLFLAASLSAQN-----EGWDSPICTEGVSVSWGENT 51
Db  620 QACPPGFWGACFACSHCHN-----GASCSAEDGACHCTPGWTGLFCTQRCFAFFGKDC 674
Qy  52 VMSCNISNAPS--HVNIIKLRAH-----GQESAIFNEVAPGYFSRDGWQL-----QV 95
Db  675 GRVCQCGNGASCDHISGKCTCTGTGTGQHCE--QRCAPGTGYGCGQQLCECMNNSTCDHV 732
Qy  96 QGG-VAQLVIKGARDSHAGLYMHVHCHORNNRQVTLVSGAEPQSDPTGFWPVPVAVT 154
Db  733 TGTCTCSPGFGIRCDQAALMMEELNFTYKISPAL-----GAERHSV-----GAVTGIML 782
Qy  155 AVFILLVALVMFAWYRCRCQORRE 179
Db  783 LLFLIVLLGLFAWHRRRQKEGRD 807

RESULT 10
US-10-052-648A-34
/ Sequence 34, Application US/10052648A
/ Publication No. US2004000558A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, David
/ APPLICANT: Burgess, Catherine
/ APPLICANT: Casman, Stacie
/ APPLICANT: Colman, Steven
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Gunther, Erik
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: MacDougall, John R.
/ APPLICANT: Mehraban, Fuad
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Rothenberg, Mark
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Stone, David J.
/ APPLICANT: Vernet, Corine A.M.
```

```
/ APPLICANT: Zethusen, Bryan D.
/ TITLE OF INVENTION: PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
/ FILE OF INVENTION: USING THE SAME
/ FILE REFERENCE: 21402-250 (CURA-550)
/ CURRENT APPLICATION NUMBER: US/10/052,648A
/ CURRENT FILING DATE: 2002-12-09
/ PRIOR APPLICATION NUMBER: 60/262,454
/ PRIOR FILING DATE: 2001-01-18
/ PRIOR APPLICATION NUMBER: 60/272,920
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/284,549
/ PRIOR FILING DATE: 2001-04-18
/ PRIOR APPLICATION NUMBER: 60/303,229
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/262,892
/ PRIOR FILING DATE: 2001-01-19
/ PRIOR APPLICATION NUMBER: 60/263,605
/ PRIOR FILING DATE: 2001-01-23
/ PRIOR APPLICATION NUMBER: 60/269,098
/ PRIOR FILING DATE: 2001-02-15
/ PRIOR APPLICATION NUMBER: 60/264,159
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/271,855
/ PRIOR FILING DATE: 2001-02-27
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 97
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 34
/ LENGTH: 969
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-052-648A-34

Query Match          7.3%; Score 96; DB 15; Length 969;
Best Local Similarity 24.9%; Pred. No. 2.9;
Matches 51; Conservative 23; Mismatches 87; Indels 44; Gaps 10;

Qy  2 QTCPLAFPG----HVSQALGTLFLAASLSAQN-----EGWDSPICTEGVSVSWGENT 51
Db  620 QACPPGFWGACFACSHCHN-----GASCSAEDGACHCTPGWTGLFCTQRCFAFFGKDC 674
Qy  52 VMSCNISNAPS--HVNIIKLRAH-----GQESAIFNEVAPGYFSRDGWQL-----QV 95
Db  675 GRVCQCGNGASCDHISGKCTCTGTGTGQHCE--QRCAPGTGYGCGQQLCECMNNSTCDHV 732
Qy  96 QGG-VAQLVIKGARDSHAGLYMHVHCHORNNRQVTLVSGAEPQSDPTGFWPVPVAVT 154
Db  733 TGTCTCSPGFGIRCDQAALMMEELNFTYKISPAL-----GAERHSV-----GAVTGIML 782
Qy  155 AVFILLVALVMFAWYRCRCQORRE 179
Db  783 LLFLIVLLGLFAWHRRRQKEGRD 807

RESULT 11
US-10-072-012-446
/ Sequence 446, Application US/10072012
/ Publication No. US20040033493A1
/ GENERAL INFORMATION:
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Zethusen, Bryan
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shimkets, Richard
/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esha
/ APPLICANT: Padigar, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
```

RESULT 12
US-10-719-993-534
; Sequence 534, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE. METHODS OF DETECTION AND USES THEREOF

	Query Match	7.0%	Score 91.5	DB 15	Length 597
	Best Local Similarity	19.3%	Pred: No. 4.3	84	Indels 121
	Matches 62	Conservative 44	Mismatches		Gaps 16
Qy	21	FLAASLSAQNEGWDS-	-----	ICTGCVGSVSW	-----GE 49
		:	:	:	:
Db	299	FKAAAAEAGHPDWELPDD	DAGEINDT	PDTGFTFAERGT	YLTGQGRFELTWSYRKLIOHQD 358
		:	:	:	:
Qy	50	NTVMSCNISNAFSHVNIKLRA	-----	HQGESAIENEVAPGYES	-----RDGWMQLQVQ 96
		:	:	:	:
Db	359	RVLDEAN--KAFILGCKVKLA	AKVSGIHWYRHPSHAA	-----ELTSGYVNLGRDGY	-----408
		:	:	:	:

Query Match 7.0%; Score 91; DB 15; Length 6620;
Best Local Similarity 22.8%; Pred. No. 1.2e+02;
Matches 58; Conservative 34; Mismatches 102; Indels 60; Gaps 10;
QV 11 HV5QALGTLFLF LAASLSAQNGWDSPTCTGTV-----VSV5NGENTVW5CNS1SNA 60

```
Db 1779 HGAQVLDIAIY---SCRVGAEGQDFPVQVEEVAAKFCRLELPEVCGELGGTVTLACELSPA 1835
Qy 61 FSHVNIKLRAHQESAI FNEVAPGVFSRDGHQLOVGGVAOLVIKIGARDSHAGLYMMHLV 120
Db 1836 CAEVVWRC-----GNTQPRVGKR--FQVVAEGPVRSLTVLGLRAEDAGEY-----V 1879
Qy 121 GHORNR---QVTLLEV-----SGAEPQSAPDTGFMFVPVPAVTVAVFILLVALYMFAYR 170
Db 1880 CESRDDHTSAQLTVSVPRWKFMSGLSTVVAEEGGEATFQCWVSPSDVAVV-----WFR 1933
Qy 171 CRCQORREKFFLLEPOMKVAALRAGAQGLSRASAEJ-----WTPDSEPTPRPLALVF 225
Db 1934 DGA-----LLQPSEKFAISQSGASHSLTISDLVLEDAGQITVEAEGASSAALRV 1983
Qy 226 KPSPLGALLELLSPQ 239
Db 1984 REAPVLFKKKLEPQ 1997
```

Search completed: October 17, 2005, 07:56:58
Job time : 2068 secs

QY 61 FSHVNIKLRAHQESAIFNEVAPGYFSRDGWLQVQGGVAQLVKGARDSHAGLYMMHLV 120
DB 61 FSHVNIKLRAHQESAIFNEVAPGYFSRDGWLQVQGGVAQLVKGARDSHAGLYMMHLV 120
QY 121 GHORNNRQVTLVSGAEPQSDPTGFWPVPVAVTAVFILLVALVFMFAYRCRCSCQORREK 180
DB 121 GHORNNRQVTLVSGAEPQSDPTGFWPVPVAVTAVFILLVALVFMFAYRCRCSCQORREK 180
QY 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQ 240
DB 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQ 240
QY 241 LFPYAADP 248
DB 241 LFPYAADP 248

RESULT 2

US-09-210-474-1
; Sequence 1, Application US/09210474
; Patent No. 6072034
; GENERAL INFORMATION:
; APPLICANT: KAUFMAN, RUSSEL E.
; APPLICANT: SLENTZ-KESLER, KIMBERLY
; TITLE OF INVENTION: GENE PRODUCT OVER EXPRESSED IN CANCER
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/755,559
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-210-474-1

Query Match 100.0%; Score 1308; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.6e-139;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOTCPLAFPGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
DB 1 MOTCPLAFPGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
QY 61 FSHVNIKLRAHQESAIFNEVAPGYFSRDGWLQVQGGVAQLVKGARDSHAGLYMMHLV 120
DB 61 FSHVNIKLRAHQESAIFNEVAPGYFSRDGWLQVQGGVAQLVKGARDSHAGLYMMHLV 120

QY 121 GHORNNRQVTLVSGAEPQSDPTGFWPVPVAVTAVFILLVALVFMFAYRCRCSCQORREK 180
DB 121 GHORNNRQVTLVSGAEPQSDPTGFWPVPVAVTAVFILLVALVFMFAYRCRCSCQORREK 180
QY 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQ 240
DB 181 KFFLEPQMKVAALRAGAQQGLSRASAEIWTDPSEPTPRPLALVFKPSPLGALELLSPQ 240
QY 241 LFPYAADP 248
DB 241 LFPYAADP 248

RESULT 3

US-09-539-774-1
; Sequence 1, Application US/09539774
; Patent No. 6350615
; GENERAL INFORMATION:
; APPLICANT: KAUFMAN, RUSSEL E.
; APPLICANT: SLENTZ-KESLER, KIMBERLY
; TITLE OF INVENTION: GENE PRODUCT OVER EXPRESSED IN CANCER
; TITLE OF INVENTION: CELLS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/539,774
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/210,474
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-539-774-1

Query Match 100.0%; Score 1308; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.6e-139;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOTCPLAFPGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
DB 1 MOTCPLAFPGHVSQALGTLFLAASLSAQNEGWDSPICTEGVSVSWGENTVMSCNISNA 60
QY 61 FSHVNIKLRAHQESAIFNEVAPGYFSRDGWLQVQGGVAQLVKGARDSHAGLYMMHLV 120
DB 61 FSHVNIKLRAHQESAIFNEVAPGYFSRDGWLQVQGGVAQLVKGARDSHAGLYMMHLV 120
QY 121 GHORNNRQVTLVSGAEPQSDPTGFWPVPVAVTAVFILLVALVFMFAYRCRCSCQORREK 180
DB 121 GHORNNRQVTLVSGAEPQSDPTGFWPVPVAVTAVFILLVALVFMFAYRCRCSCQORREK 180

[illegible]

RESULT 7
US-09-997-165-8
; Sequence 8, Application US/09997165
; Patent NO. 6762030
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Farnslow, William C.
; TITLE OF INVENTION: LIGAND FOR CD7 AND METHODS OF USE THEREOF
; FILE REFERENCE: 2913-US
; CURRENT APPLICATION NUMBER: US/09/997,165
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: PCT/US00/14612
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/136,450
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-997-165-8

RESULT 8
 US-09-489-039A-10298
 ; Sequence 10298, Application US/09489039A
 ; Patent No. 6610836
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary Breton et. al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 ; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2004001
 ; CURRENT APPLICATION NUMBER: US/09/489,039A
 ; CURRENT FILING DATE: 2000-01-27
 ; PRIOR APPLICATION NUMBER: US 60/117,747
 ; PRIOR FILING DATE: 1999-01-29
 ; NUMBER OF SEQ ID NOS: 14342
 ; SEQ ID NO 10298
 ; LENGTH: 1171

```

; TYPE: PRNT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10298

Query Match          6.9%   Score 90.5; DB 4; Length 1171;
Best Local Similarity 22.7%; Pred. No. 1.1; Indels 61; Gaps 13;
Matches 57; Conservative 37; Mismatches 96;

QY 19 LLFLAASLSAQNEGWDSPICTEGVVS-----VSMGENTV---MSCNISNAFSHV 64
    ||||| : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 582 LAFYAASL-AASHPWRLPV-DDGLVSVQRTRLIRQLGRNSESTLYKMLAQVANQVADM 639
    ||||| : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 65 NI-KLRAHGOESAI P--NEVAPGYFRDRGHQLOVQGGAOLVTIKGARDSHAGLYMMHLVG 121
    : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 640 RLADMTADTDSARLFSFTDEVVPGMFTRQAWEQAVQPAIEKVAAE--RRDE----MDWVLSD 694
    : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 122 HORNRRQVT---LEVSGAEPQAPDPTGFWPVPVVTVTAFFLLVALVMFAWYRCRCQQOR 177
    : : | : | : | : | : | : | : | : | : | : | : | : |
Db 695 TKQTAAOSTSPEALRPALRLABRYFADFSGAW-----JDFLNLSRWQRAATLSDA 742

QY 178 REKKFFLLEPQM K--VAALRAGAQQG-----LSRASAEWLTPDSEP----- 216
    : : | : | : | : | : | : | : | : | : | : | : | : |
Db 743 IDQLTLNADVRSPLVALMNTLSVQGETGTGOTGEAIALDSL VKSAQLFNDRNSPVIDORS 802
    : : | : | : | : | : | : | : | : | : | : | : | : |

QY 217 TPRPLALVFKEP 227
    |||||
Db 803 ARGPLDATFGP 813

```

RESULT 9
US-09-252-991A-27771
; Sequence 27771, Application US/09252991A
; Patent NO. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27771
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27771

RESULT 10

```
US-09-949-016-6949
; Sequence 6949, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6949
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6949

Query Match          6.5%; Score 84.5; DB 4; Length 455;
Best Local Similarity 22.2%; Pred. No. 1.2;
Matches 41; Conservative 33; Mismatches 58; Indels 53; Gaps 10;

QY      8  FPGH-VSQALGTLFLAASLSAQNE-----GWDSPICTEGVVSVSGENTVMSNCISNAFS 62
DQ      4  FPGNLSGAVASFILLTMKQSEDFRIVGPAHPILA-GV-----GEDALLTCQLLPKRT 57

QY      63  HVNIKLRAGHGOESAFNEVAPGYFSRD-----GWQLQVOGGVAQ-----LVIK 105
DQ      58  TMHVEVRYRSEPS-----TPFVHRDGVETEMQMEYRGVWEIENGIAKGNVALKIH 112

QY      106  GARDSHAGLYMHLV-CHQRNRRQVTLVSGAEQSPAD-----TGFW 147
DQ      113  NIQPSDNGQYWCHFDQNGYCGTSLLLKVAGL--GSAPSIHMEGPGSGVOLVCTARGWF 170

QY      148  PVPVAV 152
DQ      171  PEPQV 175

RESULT 11
US-09-949-016-11026
; Sequence 11026, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11026
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11026

Query Match          6.5%; Score 84.5; DB 4; Length 455;
Best Local Similarity 22.2%; Pred. No. 1.2;
Matches 41; Conservative 33; Mismatches 58; Indels 53; Gaps 10;

QY      8  FPGH-VSQALGTLFLAASLSAQNE-----GWDSPICTEGVVSVSGENTVMSNCISNAFS 62
DQ      4  FPGNLSGAVASFILLTMKQSEDFRIVGPAHPILA-GV-----GEDALLTCQLLPKRT 57

QY      63  HVNIKLRAGHGOESAFNEVAPGYFSRD-----GWQLQVOGGVAQ-----LVIK 105
DQ      58  TMHVEVRYRSEPS-----TPFVHRDGVETEMQMEYRGVWEIENGIAKGNVALKIH 112

QY      106  GARDSHAGLYMHLV-CHQRNRRQVTLVSGAEQSPAD-----TGFW 147
DQ      113  NIQPSDNGQYWCHFDQNGYCGTSLLLKVAGL--GSAPSIHMEGPGSGVOLVCTARGWF 170

QY      148  PVPVAV 152
DQ      171  PEPQV 175

RESULT 12
US-09-430-503-46
; Sequence 46, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-46

Query Match          6.4%; Score 83.5; DB 3; Length 199;
Best Local Similarity 21.9%; Pred. No. 0.44;
Matches 34; Conservative 28; Mismatches 54; Indels 39; Gaps 6;

QY      39  TEGVSVSVW-----GENTVMSNCISNAFSHVNIKLRAGHGOESAFNEVAPGYFSRDGWL 93
DQ      66  TGLTSSVMSFQPEGADTTVS-----FFHYS-----OGQVYLGNYPPFKDRISWAG 111

QY      94  QVQGGVAQLVIKGARDSHAGLYMHL-----VGHQRNRRQVTLVSGAEQSPADPT 144
DQ      112  DLKDKASINENMQFIHNGTYICDVKNPPDIVVQPGH-----IRIYVVEKENLPVP 163

QY      145  GFVFPVAVTVAFI---LLVALYMFAYRCRCSSQ 176
DQ      164  PVMVAVGIVTAVVLGLTLLIISMILAVLYRRKNSKR 198

RESULT 13
US-09-430-503-48
; Sequence 48, Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhizhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-430-503-48
```


